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(21) International Application Number: PCT/US98/06955 (22) International Filing Date: 10 April 1998 (10.04.98) (30) Priority Data: 08/838,821 10 April 1997 (10.04.97) US (71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US). (72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US). (74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs) (57) Abstract . Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.		

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5 FIELD OF THE INVENTION

BACKGROUND OF THE INVENTION

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect.

25 Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators

30 searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent
35 discloses a "signal sequence trap" which selectively identifies ESTs for secreted

proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

5 The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

 In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

15 In other embodiments, the present invention provides an isolated polynucleotide
 consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

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 30 or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide
 comprising a nucleotide sequence which hybridizes to a sequence selected from the group
 consisting of:

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NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

10

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

15 Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

1	BV31	18	CB302	35	BZ83	52	CD244
2	BV34	19	CB318	36	BZ87	53	CD265
20 3	BV37	20	CB321	37	CB15	54	BT217
4	BV45	21	CB96	38	CB2	55	BV278
5	BV8	22	CB98	39	CB44	56	BV280
6	BV93	23	BZ42	40	CC11	57	BV282
7	BV99	24	BZ53	41	CC182	58	BV285
25 8	CB100	25	BZ56	42	CC298	59	BV286
9	CB107	26	BZ6	43	CC310	60	BV291
10	CB110	27	BZ607	44	CC323	61	BV295
11	CB114	28	BZ61	45	CC332	62	BW389
12	CB118	29	BZ62	46	CC335	63	BX135
30 13	CB123	30	BZ641	47	CC338	64	BX141
14	CB129	31	BZ644	48	CC41	65	BX148
15	CB137	32	BZ72	49	CC52	66	BZ1
16	CB239	33	BZ74	50	CD107	67	BZ16
17	CB259	34	BZ82	51	CD205	68	BZ187

	69	BZ19	103	CE159	137	CH315	171	CC194
	70	BZ205	104	CE2	138	CH325	172	CC198
	71	BZ222	105	CE347	139	BZ568	173	CC199
	72	BZ230	106	CE36	140	BZ578	174	CC205
5	73	BZ234	107	CE40	141	BZ588	175	CC215
	74	BZ244	108	CE87	142	BZ597	176	CC253
	75	BZ269	109	CG1	143	BZ598	177	CC258
	76	BZ280	110	CG44	144	CH637	178	CC259
	77	BZ288	111	CG60	145	CH644	179	CC265
10	78	BZ304	112	CG68	146	CH699	180	CC288
	79	BZ328	113	BP202	147	CI240	181	CC95
	80	BZ331	114	BP242	148	CI247	182	CC96
	81	BP646	115	BP243	149	CJ1	183	CD311
	82	BP652	116	BZ444	150	CJ19	184	CD323
15	83	BP656	117	BZ453	151	CJ24	185	CH338
	84	BP666	118	CC233	152	CJ27	186	CH355
	85	BP667	119	CC242	153	CJ3	187	CH377
	86	BP674	120	CC247	154	CJ37	188	CH421
	87	BP695	121	CC344	155	CJ42	189	CH425
20	88	BP705	122	CC346	156	CJ44	190	CH522
	89	BP713	123	CC351	157	CJ49	191	CH541
	90	BP720	124	CC359	158	CJ50	192	CH555
	91	BP750	125	CC364	159	CJ55	193	CH558
	92	BP754	126	CC365	160	CJ6	194	CH582
25	93	BW143	127	CC374	161	CJ76	195	CH595
	94	BR307	128	CE303	162	CJ77	196	CH720
	95	BR309	129	CE328	163	CJ84	197	CH723
	96	BR312	130	CG199	164	CJ86	198	CH724
	97	BR318	131	CG209	165	CJ91	199	CH735
30	98	CB187	132	CG210	166	CC111	200	CH742
	99	CB190	133	CG350	167	CC118	201	CI126
	100	CB204	134	CG354	168	CC120	202	CI129
	101	CB213	135	CG426	169	CC126	203	CI133
	102	CE120	136	CH303	170	CC130	204	CI181

	205	CI229	239	CG160	273	CI395	307	CJ397
	206	CI25	240	CG175	274	CI407	308	CJ400
	207	CI52	241	CG176	275	CI411	309	CJ404
	208	CI84	242	CG180	276	CI437	310	CJ415
5	209	CI91	243	CG279	277	CI443	311	CJ420
	210	BP163	244	CG292	278	CI444	312	CJ424
	211	BP175	245	CG300	279	CI459	313	CJ434
	212	BP199	246	CG301	280	CI480	314	CJ454
	213	BP272	247	CG314	281	CI490	315	CJ457
10	214	BP284	248	CG315	282	CI492	316	CJ481
	215	BP294	249	CG324	283	CI493	317	CJ493
	216	BP299	250	CG336	284	CI510	318	CJ501
	217	BP300	251	CG99	285	CI522	319	CJ514
	218	BP306	252	CH143	286	CI534	320	CJ539
15	219	BP311	253	CH207	287	CI542	321	CJ540
	220	BP312	254	CH224	288	CI560	322	CJ549
	221	BP327	255	CH227	289	CI561	323	CJ551
	222	BP345	256	CH245	290	CI583	324	CK126
	223	BP368	257	CH246	291	CI586	325	CK151
20	224	BP467	258	CH27	292	CJ145	326	CK181
	225	BP468	259	CH30	293	CJ149	327	CK201
	226	BR375	260	CH4	294	CJ160	328	CK213
	227	BR390	261	CH64	295	CJ164	329	CK218
	228	BR408	262	CH78	296	CJ168	330	CK234
25	229	BR418	263	CH85	297	CJ176	331	CK37
	230	BY66	264	CH87	298	CJ183	332	CK48
	231	CF118	265	CN320	299	CJ194	333	CL104
	232	CF127	266	CN343	300	CJ206	334	CL110
	233	CF22	267	CN344	301	CJ230	335	CL122
30	234	CF235	268	CN395	302	CJ237	336	CL132
	235	CG109	269	CN423	303	CJ257	337	CL147
	236	CG131	270	CI363	304	CJ265	338	CL152
	237	CG153	271	CI386	305	CJ378	339	CL181
	238	CG158	272	CI392	306	CJ389	340	CL182

	341	CL399	375	CN516	409	CO58	443	CO155
	342	CL469	376	CN532	410	CO48	444	CO153
	343	CL470	377	CN552	411	CO444	445	CO145
	344	CL481	378	CN593	412	CO431	446	CO140
5	345	CL493	379	CN619	413	CO391	447	CO139
	346	CM12	380	CN621	414	CO384	448	CO128
	347	CM178	381	CN667	415	CO36	449	CO1254
	348	CM188	382	CN703	416	CO351	450	CO1247
	349	CM194	383	CN718	417	CO337	451	CO1232
10	350	CM246	384	CN729	418	CO327	452	CO1224
	351	CM251	385	CN835	419	CO315	453	CO1223
	352	CM54	386	CN896	420	CO304	454	CO1206
	353	CM62	387	CO933	421	CO270	455	CO1198
	354	CN140	388	CO924	422	CO268	456	CO1196
15	355	CN171	389	CO908	423	CO264	457	CO1194
	356	CN173	390	CO900	424	CO261	458	CO1187
	357	CN238	391	CO889	425	CO257	459	CO1180
	358	CN29	392	CO888	426	CO253	460	CO1178
	359	CN291	393	CO874	427	CO25	461	CO1175
20	360	CN304	394	CO851	428	CO246	462	CO117
	361	CN327	395	CO83	429	CO244	463	CO1168
	362	CN49	396	CO821	430	CO240	464	CO1164
	363	CN50	397	CO806	431	CO228	465	CO1162
	364	CN54	398	CO798	432	CO223	466	CO1161
25	365	CN65	399	CO79	433	CO222	467	CO1159
	366	CJ305	400	CO71	434	CO209	468	CO1153
	367	CJ316	401	CO7	435	CO205	469	CO1151
	368	CJ317	402	CO69	436	CO204	470	CO1137
	369	CJ336	403	CO66	437	CO20	471	CO1123
30	370	CJ347	404	CO639	438	CO197	472	CO1076
	371	CJ360	405	CO638	439	CO185	473	CO1072
	372	CJ365	406	CO625	440	CO170	474	CO1026
	373	CJ366	407	CO62	441	CO17	475	CO1000
	374	CN483	408	CO602	442	CO163	476	CN755

	477	CN736	511	CR1166	545	CR632	579	CO409
	478	CN709	512	CR1186	546	CR641	580	CO474
	479	CO975	513	CR1190	547	CT729	581	CO480
	480	CO990	514	CR329	548	CN922	582	CO500
5	481	CP280	515	CR354	549	CN934	583	CO519
	482	CP283	516	CR377	550	CN951	584	CO522
	483	CP287	517	CR390	551	CN952	585	CO526
	484	CP289	518	CR392	552	CN980	586	CO559
	485	CP294	519	CR422	553	CP111	587	CO595
10	486	CP304	520	CR423	554	CP147	588	CO605
	487	CP307	521	CR466	555	CU13	589	CO618
	488	CP311	522	CR477	556	CP251	590	CO629
	489	CP313	523	CR478	557	CP258	591	CO643
	490	CP314	524	CR482	558	CP33	592	CO653
15	491	CP328	525	CR491	559	CP41	593	CO661
	492	CP352	526	CR494	560	CP91	594	CO667
	493	CQ286	527	CR502	561	CP92	595	CO695
	494	CQ294	528	CR506	562	CQ160	596	CO696
	495	CQ304	529	CR513	563	CQ165	597	CO707
20	496	CQ309	530	CR514	564	CQ268	598	CO716
	497	CQ331	531	CR515	565	CQ30	599	CO718
	498	CQ333	532	CR527	566	CR100	600	CO720
	499	CR1116	533	CR529	567	CR178	601	CO722
	500	CR1118	534	CR537	568	CR184	602	CO736
25	501	CR1121	535	CR538	569	CR263	603	CO763
	502	CR1127	536	CR540	570	CR335	604	CO767
	503	CR1135	537	CR541	571	CR4	605	CP116
	504	CR1141	538	CR545	572	CR61	606	CP151
	505	CR1142	539	CR587	573	CR93	607	CI293
30	506	CR1144	540	CR588	574	CO282	608	CI294
	507	CR1147	541	CR593	575	CO310	609	CI298
	508	CR1155	542	CR594	576	CO334	610	CU14
	509	CR1156	543	CR611	577	CO387	611	CU2
	510	CR1162	544	CR618	578	CO390	612	CU25

	613	CU32	647	CR678	681	CT748	715	CS520
	614	CU39	648	CR726	682	CT738	716	CS524
	615	CU40	649	CR733	683	CT726	717	CS534
	616	DA10	650	CR778	684	CT706	718	CT14
5	617	DA136	651	CR836	685	CT705	719	CT142
	618	DA155	652	CR839	686	CT702	720	CT143
	619	DA16	653	CR872	687	CT693	721	CT149
	620	DA165	654	CR890	688	CT677	722	CT156
	621	DA170	655	CR916	689	CT658	723	CT159
10	622	DA183	656	CR929	690	CT645	724	CT162
	623	DA223	657	CR930	691	CT636	725	CT188
	624	DA224	658	CR936	692	CT631	726	CT189
	625	DA225	659	CR974	693	CT616	727	CT190
	626	DA227	660	CT747	694	CT611	728	CT193
15	627	DA228	661	CT727	695	CT600	729	CT194
	628	DA234	662	CT690	696	CT585	730	CT2
	629	DA244	663	CT649	697	CT583	731	CT207
	630	DA246	664	CT624	698	CS224	732	CT220
	631	DA274	665	CT564	699	CS255	733	CT223
20	632	DA471	666	CT88	700	CS267	734	CT226
	633	DA490	667	CT864	701	CS271	735	CT227
	634	DA495	668	CT857	702	CS278	736	CT24
	635	DA496	669	CT852	703	CS284	737	CT254
	636	DA504	670	CT838	704	CS296	738	CT256
25	637	DA505	671	CT808	705	CS297	739	CT258
	638	DA507	672	CT807	706	CS317	740	CT271
	639	DA516	673	CT797	707	CS319	741	CT275
	640	DA529	674	CT791	708	CS322	742	CT28
	641	DA84	675	CT785	709	CS353	743	CT284
30	642	CR1003	676	CT783	710	CS366	744	CT293
	643	CR1013	677	CT780	711	CS471	745	CO1020
	644	CR1044	678	CT771	712	CS475	746	CO1043
	645	CR1056	679	CT754	713	CS485	747	CO1067
	646	CR1063	680	CT750	714	CS516	748	CO1069

	749	CO1080	783	DB257	817	CW1617	851	CT384
	750	CO1081	784	DB343	818	CW1632	852	CT392
	751	CO1094	785	DB415	819	CW1636	853	CT394
	752	CO956	786	DB53	820	CW1640	854	CT415
5	753	CO973	787	DB85	821	CW169	855	CT421
	754	CJ471	788	CW1000	822	CW172	856	CT423
	755	CJ472	789	CW1038	823	CW173	857	CT434
	756	CJ475	790	CW1087	824	CW175	858	CT440
	757	CJ483	791	CW1100	825	CV123	859	CT443
10	758	CJ484	792	CW1109	826	CV156	860	CT450
	759	CJ485	793	CW1112	827	CV160	861	CT453
	760	CJ486	794	CW115	828	CV192	862	CT457
	761	CJ488	795	CW1150	829	CV203	863	CT466
	762	CJ496	796	CW1155	830	CV215	864	CT474
15	763	CJ497	797	CW1177	831	CV227	865	CT475
	764	CJ498	798	CW1195	832	CV263	866	CT479
	765	CJ507	799	CW1200	833	CV275	867	CT489
	766	CJ508	800	CW1201	834	CV305	868	CT51
	767	CJ519	801	CW1214	835	CV328	869	CT519
20	768	CJ520	802	CW1225	836	CV380	870	CT521
	769	CJ521	803	CW1230	837	CV394	871	CT526
	770	CJ522	804	CW1233	838	CV410	872	CT536
	771	CJ534	805	CW1272	839	CV416	873	CT541
	772	CJ536	806	CW1292	840	CV461	874	CT547
25	773	CJ543	807	CW1306	841	CV493	875	CT550
	774	CJ544	808	CW1311	842	CV501	876	CT559
	775	CJ547	809	CW1314	843	CT3	877	CT562
	776	CK53	810	CW1334	844	CT314	878	DE36
	777	CK7	811	CW1365	845	CT317	879	DE37
30	778	CK70	812	CW1372	846	CT320	880	DE4
	779	CL49	813	CW149	847	CT326	881	DE42
	780	CL63	814	CW152	848	CT340	882	DE63
	781	DB203	815	CW1574	849	CT353	883	DE70
	782	DB208	816	CW1611	850	CT358	884	DE83

	885	DE103	919	CS771	953	CW775	987	DA337
	886	DE105	920	CS773	954	CW795	988	DA348
	887	DE110	921	CS776	955	CW802	989	DA373
	888	DE114	922	CW222	956	CW823	990	DA388
5	889	DE117	923	CW224	957	CW835	991	DA389
	890	DE119	924	CW226	958	CZ115	992	DA390
	891	DE91	925	CW232	959	CZ122	993	DA391
	892	DE95	926	CW254	960	CZ186	994	DA414
	893	DE96	927	CW272	961	CZ214	995	DA428
10	894	CW420	928	CW280	962	CZ247	996	DA443
	895	CW424	929	CW313	963	CZ251	997	DA451
	896	CW457	930	CW314	964	CZ268	998	CW1458
	897	CW485	931	CW347	965	CZ270	999	CW1475
	898	CS383	932	CW354	966	CZ278	1000	CW1481
15	899	CS384	933	CW363	967	CZ291	1001	CW1506
	900	CS399	934	CW374	968	CZ320	1002	CW1510
	901	CS405	935	CW382	969	CZ326	1003	CW1543
	902	CS409	936	CW383	970	CZ362	1004	CW1550
	903	CS431	937	CW386	971	CW1414	1005	CW1552
20	904	CS438	938	CW388	972	CW1440	1006	CZ372
	905	CS454	939	CW512	973	CE209	1007	CZ374
	906	CS588	940	CW517	974	CE216	1008	CW902
	907	CS629	941	CW53	975	CE232	1009	CW922
	908	CS636	942	CW554	976	CE242	1010	CW924
25	909	CS637	943	CW585	977	CF193	1011	CW976
	910	CS638	944	CW618	978	CH776	1012	CW979
	911	CS645	945	CE197	979	CW1381	1013	CW984
	912	CS679	946	CW662	980	CW1389	1014	CW998
	913	CS682	947	CW675	981	CW1399	1015	CZ1
30	914	CS734	948	CW691	982	CZ653	1016	CW753
	915	CS743	949	CW707	983	CZ681	1017	CW759
	916	CS752	950	CW735	984	CZ711	1018	CW800
	917	CS756	951	CW762	985	CZ719	1019	CW891
	918	CS765	952	CW768	986	DA306	1020	CW960

	1021	CT80	1055	DC14	1089	DH1206	1123	DF478
	1022	DF1115	1056	CW1670	1090	DH1212	1124	DF483
	1023	DF1117	1057	CW1682	1091	DH1213	1125	DF494
	1024	DF1125	1058	DF814	1092	DH190	1126	DF499
5	1025	DF134	1059	DF821	1093	DI191	1127	DF7
	1026	DF14	1060	DF842	1094	DI207	1128	DF706
	1027	DF163	1061	DG1	1095	DI216	1129	DF713
	1028	DF174	1062	DG17	1096	DI243	1130	DF727
	1029	DF175	1063	DG174	1097	DI248	1131	DF737
10	1030	DF180	1064	DG256	1098	DI261	1132	DF756
	1031	DF185	1065	DG26	1099	DF1005	1133	DF757
	1032	DF201	1066	DG266	1100	DF1009	1134	DF762
	1033	DF202	1067	DG326	1101	DF1010	1135	DF776
	1034	DF203	1068	DG327	1102	DF102	1136	DF777
15	1035	DF206	1069	DG329	1103	DF1050	1137	DF780
	1036	DF219	1070	DG330	1104	DF1062	1138	DF783
	1037	DF230	1071	DG331	1105	DF1063	1139	DG12
	1038	DF232	1072	DG44	1106	DF1084	1140	DG121
	1039	DF239	1073	DG65	1107	DF153	1141	DG128
20	1040	DF244	1074	DG69	1108	DF218	1142	DG141
	1041	DF259	1075	DG7	1109	DF251	1143	DG149
	1042	DF266	1076	DG71	1110	DF280	1144	DH28
	1043	DF46	1077	DG76	1111	DF286	1145	DH303
	1044	DF65	1078	DG82	1112	DF316	1146	DH318
25	1045	DF69	1079	DH1086	1113	DF317	1147	DH322
	1046	DB145	1080	DH1098	1114	DF343	1148	DH340
	1047	DB150	1081	DH1135	1115	DF347	1149	DH371
	1048	DB159	1082	DH1145	1116	DF370	1150	DH40
	1049	DB174	1083	DH1153	1117	DF382	1151	DH401
30	1050	DB180	1084	DH1182	1118	DF396	1152	DH432
	1051	CY1	1085	DH1185	1119	DF428	1153	DH451
	1052	CY11	1086	DH1190	1120	DF453	1154	DH496
	1053	CY3	1087	DH1191	1121	DF457	1155	DH502
	1054	CY9	1088	DH1201	1122	DF460	1156	DH529

	1157	DH66	1191	DF915	1225	DH1357	1259	DI501
	1158	DF518	1192	DF948	1226	DH145	1260	DI504
	1159	DF521	1193	DF950	1227	DH999	1261	DK111
	1160	DF538	1194	DF956	1228	DI160	1262	DK113
5	1161	DF543	1195	DF966	1229	DI386	1263	DK120
	1162	DF545	1196	DF968	1230	DI391	1264	DK122
	1163	DF547	1197	DF971	1231	DI435	1265	DK126
	1164	DF568	1198	DF973	1232	DI448	1266	DK134
	1165	DF587	1199	DF979	1233	DI454	1267	DK136
10	1166	DF589	1200	DF984	1234	DJ109	1268	DK150
	1167	DF591	1201	DF989	1235	DJ146	1269	DK160
	1168	DF601	1202	DH1257	1236	DJ167	1270	DK170
	1169	DF606	1203	DH1308	1237	DF1065	1271	DK182
	1170	DF62	1204	DH1314	1238	DI387	1272	DK185
15	1171	DF620	1205	DI341	1239	DI393	1273	DK197
	1172	DF625	1206	DH1265	1240	DI403	1274	DK206
	1173	DF648	1207	DI349	1241	DI430	1275	DK219
	1174	DF657	1208	DI355	1242	DI438	1276	DK223
	1175	DF659	1209	DI362	1243	DJ2	1277	DK227
20	1176	DF661	1210	DI366	1244	DJ188	1278	DK229
	1177	DF662	1211	DI508	1245	DJ238	1279	DK230
	1178	DF670	1212	DI516	1246	DJ259	1280	DK243
	1179	DF674	1213	DI518	1247	DK64	1281	DK264
	1180	DF682	1214	DF1066	1248	DK70	1282	DK268
25	1181	DF688	1215	DF1069	1249	DK81	1283	DK31
	1182	DF810	1216	DG279	1250	DK84	1284	DK39
	1183	DF823	1217	DH1010	1251	DI462	1285	DK93
	1184	DF835	1218	DH1013	1252	DI466	1286	DL101
	1185	DF860	1219	DH1044	1253	DI474	1287	DL110
30	1186	DF877	1220	DH1045	1254	DI475	1288	DL116
	1187	DF883	1221	DH1073	1255	DI479	1289	DL132
	1188	DF895	1222	DH1078	1256	DI480	1290	DL63
	1189	DF909	1223	DH1340	1257	DI482	1291	DL82
	1190	DF910	1224	DH1349	1258	DI500	1292	DL95

	1293	DL99	1327	DL491	1361	DL547	1395	DO181
	1294	DJ332	1328	DL495	1362	DL550	1396	DO419
	1295	DJ362	1329	DL498	1363	DL551	1397	DO424
	1296	DK290	1330	DL504	1364	DL601	1398	DO440
5	1297	DK321	1331	DM118	1365	DL604	1399	DO447
	1298	DK324	1332	DM122	1366	DL605	1400	DO568
	1299	DK329	1333	DM126	1367	DL607	1401	DO575
	1300	DK357	1334	DM128	1368	DL608	1402	DO589
	1301	DK360	1335	DM130	1369	DL616	1403	DO610
10	1302	DL141	1336	DM147	1370	DL619	1404	DO715
	1303	DL146	1337	DM169	1371	DL620	1405	DO722
	1304	DL162	1338	DM26	1372	DL634	1406	DO737
	1305	DL163	1339	DM404	1373	DM194	1407	DO742
	1306	DL169	1340	DM406	1374	DM197	1408	DO755
15	1307	DL181	1341	DM407	1375	DM221	1409	DO765
	1308	DL185	1342	DM420	1376	DM248	1410	DO797
	1309	DL218	1343	DM425	1377	DM250	1411	DO836
	1310	DL220	1344	DM435	1378	DM262	1412	DO884
	1311	DL248	1345	DM445	1379	DM265	1413	DO896
20	1312	DL289	1346	DM449	1380	DM272	1414	CZ549
	1313	DL290	1347	DM459	1381	DM278	1415	CZ598
	1314	DL291	1348	DM462	1382	DM293	1416	DT431
	1315	DL316	1349	DM469	1383	DM303	1417	DT443
	1316	DL320	1350	DM482	1384	DM340	1418	DT446
25	1317	DL321	1351	DM6	1385	DM360	1419	DT449
	1318	DL425	1352	DM94	1386	DM365	1420	DT450
	1319	DL426	1353	DJ279	1387	DM522	1421	DT455
	1320	DL427	1354	DJ284	1388	DM533	1422	DT458
	1321	DL439	1355	DJ299	1389	DM542	1423	DN106
30	1322	DL440	1356	DJ319	1390	DM87	1424	DN153
	1323	DL444	1357	DJ323	1391	DN124	1425	DN176
	1324	DL457	1358	DL531	1392	DN144	1426	DT530
	1325	DL463	1359	DL535	1393	DN147	1427	DT534
	1326	DL466	1360	DL543	1394	DN167	1428	DT535

	1429	DT544	1463	DW1	1497	BK5
	1430	DT563	1464	DW389	1498	BK504
	1431	DT584	1465	DW398	1499	BK513
	1432	DT590	1466	DW654	1500	BK517
5	1433	DT596	1467	DW659		
	1434	DT597	1468	DW665		
	1435	DT598	1469	DW694		
	1436	DT640	1470	DW705		
	1437	DT655	1471	DW716		
10	1438	DT674	1472	DW749		
	1439	DT719	1473	DW761		
	1440	DT734	1474	DW765		
	1441	DT779	1475	DW771		
	1442	DT801	1476	DW78		
15	1443	DT802	1477	DW780		
	1444	DN696	1478	BK10		
	1445	DN697	1479	BK11		
	1446	DN704	1480	BK2		
	1447	DN710	1481	BK368		
20	1448	DN711	1482	BK373		
	1449	DN714	1483	BK374		
	1450	DN721	1484	BK375		
	1451	DN722	1485	BK384		
	1452	DN732	1486	BK402		
25	1453	DN740	1487	BK410		
	1454	DN746	1488	BK415		
	1455	DN747	1489	BK425		
	1456	DN753	1490	BK427		
	1457	DN756	1491	BK436		
30	1458	DN764	1492	BK445		
	1459	DN770	1493	BK455		
	1460	DN772	1494	BK458		
	1461	DN1120	1495	BK494		
	1462	DU372	1496	BK498		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,
25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table I below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) ¹	Hybridization Temperature and Buffer ²	Wash Temperature and Buffer ²
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	< 50	T _B *; 1xSSC	T _B *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T _F *; 1xSSC	T _F *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	< 50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T _J *; 4xSSC	T _J *; 4xSSC
15	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T _L *; 2xSSC	T _L *; 2xSSC
	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T _N *; 6xSSC	T _N *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T _R *; 4xSSC	T _R *; 4xSSC

²: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

³: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_b - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log [Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

5 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

10 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any
15 bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

20 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art,
25 as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting
30 expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention
5 may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

10 The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or
15 which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding
20 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related
25 DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-
30 DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -

5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:

10 *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.

15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune

20 suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may

25 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course,

30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other
5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune
10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from
15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding
10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor
20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection
25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or
30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected
5 with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured
10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-
15 3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa
20 et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching
25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

30 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma
15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of
20 progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

 Another category of tissue regeneration activity that may be attributable to the
25 protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein
30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or
5 progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural
10 cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized
15 neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from
20 chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

25 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of
30 fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,
20 alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

5 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can
15 stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one
25 cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al. Eur. J. Immunol. 25: 1744-1748; Gruber et al.
30 J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A
5 protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

- A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors
20 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.
- 25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- Suitable assays for receptor-ligand activity include without limitation those
30 described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

20 In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

30 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the
5 fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent
10 behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for
15 example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

20

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a
5 composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the
10 invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or
15 use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects
20 of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric
25 or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T
30 lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, 10 diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15 As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a 25 mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also
5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and
10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices
15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such
20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1 or 2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	Peripheral Blood Mononuclear Cell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	Salivary Gland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	Peripheral Blood Mononuclear Cell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
McCoy, John
LaVallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCC	TTCATGGCCT	AAGTGTTTAA	ATTATAAGCT	GGTGAAGTGA	AATAACACAA	60
ATCAAGCTCA	CCAATTTTAA	TACTCAGCTG	TTGATAAACA	ACACTGAAGA	GTGACATTTA	120
AATTTGAATT	ATCTTCTTTG	AAGTAGCATT	GCAGCACTTT	TGAATGACTT	CCAAAAGGCT	180
GATCATAAAA	ATCACTTCAA	TCATTTTCAA	ATTTTACTTT	AGCAGCAATG	AAGTTATTTG	240

GTATGACTCA GATGAACCTT CTGCTCTGTC TTGGAGTTAT TATGGTCATT TCATTTTCTG 309
CAACCTGGGA AAACCTCGAG 329

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCC TTCATGGCCT ACGAGTGGAT CTGGTTGAGA GGAAAGCAGC TAAAAATACA 60
GGAGATGAAA GGGATCATAA CGAACATAAT GAACCATGTT CATTATGGTT CGTGGGGAGG 120
CAGGAAAGCA CAGTATCCAG GGCATAGGCA GAAGAGCTGT CTTTCACGGG AGGAGGGGAA 180
CATATTCTAC TGCAATAAGC AAGGGCGGGG TAAGTACGGA TCGGGTACTT TGGGAACATAT 240
GACGGTAGGG AGTTCAGGAA GTTGCTGCCT GAAGGCATAA AGGTTTTTTT TTTTTTTTTT 300
TTTTTTTGCC AATTGGTCCA GTACCCTCCT TCTGTGGCCC CCATCTCCAG TCTCGAG 357

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCTTA TATAATTGG ATACCTACTC ATTGTCAGTT GTATGCTTTG CAAATATCTT 60
TCCTGACCCT TACTTACCTT TTCACTCTTA ATGGTATCTT TGATGAATCA AAAATTTTTC 120
TTTTTTTGTT GTTTTTTGAG ACAGAGTCTT AACTCTGTCA CCCAGGCTGG AGTGCAATGC 180
ATGAACATGG CTCACTGCAG CCTCACTTC TTGGAATCAA GCAATCCTCC TGCCTCAGAA 240
CCTCTCGAG 262

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAGCTCCTT TCCTTCTACT CTCCTGCTCA 60
GACCATTAGT AGGTACTTTG TTAAATAAAA AACTAGATTA ACATCAATAT TACTCCAATT 120
TGGTATCTTT TAACTATGT ATTATACCTA CTTCTTTTT ATTTCATTTA CAAATAGTTT 180
AAATTACTTT ATCAACCAGC TGTATTGTTT CCCTCTTGTA AAAGTACCAT CAAGTGGGGA 240
AAATGTATGT GGCAGTCTCG AG 262

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GAATTCGGCC TTCATGGCCT AATAACTTAC CCAGTCACGA ATATTTCTTC ATAGCAGCAT      60
CAGAGTGGAC TAATACGATT ATAATTATCA TCACCTTTTG ACTGACCAAT TGATTACAG      120
TATTGAGTTC AATCTGTTTT TTTAAAAAAT ATCTTCTAAA TATCAGGTGC TGTATTAGAT      180
GTGGGGTACA AAAATGTATT TTCATTACT CACTAATTTA CTTAAATTT ATTTATTGAG      240
GTACCTCGAG                                         250

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

GAATTCGGCC TTCATGGCCT AGGTGCTGGA AGTAAGCTGT GTGAACAAAT GAGACGATTC      60
CCCTTTCTAA TGAGTTTATA TGCAATGTGG TATCTTTACC GATACATGCT CTGTCAGAAA      120
GAAGCAGCCC ACTTCTGTCC AATAGCCAAT CCGGCTTCAG GAGCAGCAGG AGAGGCTTCG      180
GGAACGGGAG AAGAGGCTTC AGCAGCTGGC CGAGCCACAG AGCGACTTGG AGGAGCTGCA      240
CGAGAACAAG AGCGCACTGC AGTTGGAGAG CTCGAG                                         276

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

GAATTCGGCC TTCATGGCCT ACTCATTCCA AAATAAAAAA AAAAATTTCC CATGATCTTA      60
TCTAGCTTCT CTAGCAGTAC TTGTATGATT TCACCTTTCT TTCTTTATTC TTTTCTTCCA      120
TATTTTTTTT TTTTGAGACA GGGTCTCACT CTATTGTCCA GGCTAGAGTG CAGTAGTTTG      180
ATCATGACTC ACTCTAACCT GGACCTCCGG GGCCTAAGTA ATCTTCCCAC CTCAGCCTCT      240
CAAGTAGCTG GGA CTACAGG GATGTACCAC CATGCCTGGC TAAG                                         284

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGAATTCT AGACCTGCCT CGAGGACGCC AGGGAAGTGA GTTGAAAATC TGAAAATGCG	60
GCCATGGACT GGTTCCTGGC GTTGGATTAT GCTCATTCTT TTTGCCTGGG GGACCTTGCT	120
GTTTTATATA GGTGGTCACT TGGTACGAGA TAATGACCAT CCTGATCACT CTAGCCGAGA	180
ACTGTCCAAG ATTCTGGCAA AGCTTGAACG CTTAAAACAG CAGAATGAAG ACTTGAGGCC	240
AATGGCCGAA TCTCTCCGGA TACCAGAAGG CCCTATTGAT CAGGGGCCAG CTATAGGAAG	300
AGTGCGCGTT TTAGAAGAGC AGCTTGTTAA GGCCAAAGAA CAGATTGAAA ATTACAAGAA	360
ACAGACCAGA AATGGTCTGG GGAAGGATCT CGAG	394

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGTGATGA AAATGCTTTA TGCTTCAACA CTGTTGGAGG ACACAACTGT GTTTGCAAGC	60
CGGGCTATAC AGGGAATGGA ACGACATGCA AAGCATTTTG CAAAGATGGC TGTAGGAATG	120
GAGGAGCCTG TATTGCCGCT AATGTGTGTG CCTGCCACCA AGGCTTCACT GGACCCAGCT	180
GTGAAACGGA CATTGATGAA TGCTCTGATG GTTTTGTTC AATGTGACAGT CGTGCTAATT	240
GCATTAACTT GCCTGGATGG TACCACTGTG AGTGCAGAGA TGGCTACCAT GACAATGGGA	300
TGTTTTCACT AAGTGGAGAA TCGTGTGAAG ATATTGATGA GTGTGGGACC ACTCGAG	357

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCC TTCATGGCCT ATTTCCGATC TATGTATCTG TACTCATACA GCCTCATCGG	60
GCTAAACAGC CTTCTTTTCA GAACAGTAGA TCACTCAACT GGGTTTTC AA GTGACTGTTT	120
ACCTTTCAAG GCTGGCTTTA TAGGTCTTGC CTCACGTAT CCAGCAATCC AAACTTTACC	180
CTATCCCAGT CAGGACTGCA CACCTCATAT TGAAAGACAT ACCTTAGAAC CAGACTCCCC	240
AAACCTTACA AATATCCAC CTTGACTCC CGTTCTCGAG	280

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTAGA	CCTGCCTCGA	GCGCCACACA	GTGACTGCCG	GGTAAAGTTG	TGGAATTACG	60
TCCCTGGACT	CACCCCCTGC	CTTCCTCGCC	GAGTCCTGGC	CATAAAGGGC	CGCGCCACCA	120
CCCTGCCCTG	ACCCTCCCCA	ACTCTCCCTG	TCTCCTCTTT	CATTCTTCCC	CTCTTTCCTT	180
TTCCCTCTCT	TTCCCCACTT	CGATATGAGC	TGCTTCTTAA	CGGTATGAGA	TTATTTNACT	240
CCTTCTTCTT	CCTTTCCTT	CCTGTCTGTC	CTGGCCTAGA	GAGGTGCCCT	GCCTGTCCCT	300
CCTGCACCCA	CGTCCCTTT	CCAAGCATGA	ACAGTGGGAC	AGGCCCCAGG	AGATGGGTGC	360
CAGGGAGCAG	AAGGGGGAGC	CTTCAGGCCT	GGACAAAACG	AAACACCCCC	CCAAAAAAG	420
NAAACCCACG	ACTCGAG					437

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTTCTTCTA	AGTAGATCTT	CCTTCCCAT	TAAACTAGGT	TTTCTACTGC	AAGATATTTT	60
GTGCATTGCT	GTTTTAAACC	CTTTTAACAG	CGAATCATAG	CAGTCTAAGA	AGTCTTCTGA	120
ACCATCCTGG	ACTCTTGGTG	TGATTTTAAA	TTGTGTCTAC	AAGTTCTCTG	ACATTCTTCC	180
CACCAAGAGG	TAGAGTCTGT	TTCCCCTCCC	TTGAACTTA	GGTAGGCCTT	TGTTACTGCC	240
TTGATGAATA	CAATGAGACT	CGAG				264

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTTTTTAC	CCAAAGCTCT	GGAATTGTAC	ATTATTTTTT	TAAAACTCAA	AGAGGGAAAG	60
AGCCTTGTAT	CATATGTGAA	CATTGTATCA	TAGGTAATGT	TGTACAGACC	CTTTTATACA	120
GTGATCTGTC	TTGTTCTGTC	AGCAAAAATC	CTCTATGGAC	ATAGGAGGTG	CTGTGTCCCA	180
TGCCCTCTTG	CCCTGACAGT	GTCCCATGGG	CCCCCTTCTG	CTCCCTGCCC	CCTCCCTGCT	240
ACTGCTGATG	CACTCCCCCC	CCTCGAG				267

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GAATTCGGCC TTCATGGCCT ATTTTATT TGTGTTGTTT TGTGTTGTTG GGATGGGGTT      60
TGCCTGTGTT GCCCAGGCTG GTTTCGAATT TTTGGGCTTA TGCAATCCAC CCACCTTGGC      120
CTCCCAAAGT GCAGGGATTA CAGGCATGAG CCATCTTGCT GGGCCACCTT TTTCTTCTCT      180
TTTAACAAAT TCAGCAATTT TTCAGTCCCA GAAATCTGTA AATACATTTT TTGTGAAAAA      240
ATACAATGGG AATGGCATCA AAAGATGGTT TCTATTAGGA ATGGGAACAG GTAACAGTTT      300
TCCCTGCCAC CTCAACAATC TCGAG                                           325

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GGGCTGGCAG GCGGGCCAAA GGTAATGAAG CAAAGAGAGA GGGAAAAGAC GTGTGAAAAT      60
TGCAGAGGGG GTGACCGAGG GAAACACGTG AGCGTGATAA TGACAGAAAA ACCACGGAAG      120
GAGCAAACCT GGGCAGGGGG TGGGAAACCC GGGCCGTTTC CAGGGAGCAC AGGCAGACTC      180
AGAGGTAACA CTCAAAGCA ACAACAGAAG CAAGGAGGAA GTGGGAAAAT ATTTTAAATG      240
TGCTACAACG AAACAGCTGC CTGAATTCTA TATACCTCTT GAAAAATAATC TGCACATAAA      300
ATGGGAAAGC TTCACCGCAG CAGACCCAC TCGAG                                           335

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GAATTCGGCC TTCATGGCCT ATGCTTCTTC CACGCACCAC CACCACCACC ACCACCATCA      60
TGCCCATAGC CACGGTGGCC TGGGGTGCT GCCTGATGGG CAGTCCAAGC TCCAGGCCCT      120
GCATGCCAG TATTGCCAAG GACCGGGCCC TGCCCCGCCA CCCTACCTCC CACCCAGCA      180
GCCCTCTCTT CCCCACCTC CCCAGCAGCC CCCACCCTTG CCCCACCTGG GCTCCATTCC      240
ACCGCCTCCC GCCTCAGCCC CACCTGTGGG GCCACATGCG CACTTCCACG CCCATGGCCC      300
AGTCCCAGGG CCCCAACACT ATACCTTGGG CCGGCCAGGC AGGGCACCCA GACGGGGGGC      360
TGGAGGACAC CCTCAGTTTG CTCCACATGG CCGCCACCCC CTGCACCAGC CCACATCCCC      420
ACTGCCCCTG TACAGTCCTG CCCCCAGCA CCCTCCAGCC CACAAACAGG GCCCTAAGCA      480
CTTCATCTTC AGCCACCACC CATCTCGAG                                           509

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

GAATTCGGCC TTCATGGCCT AAAGATGGCG GAGAACAGCG GTCGCGCCGG CAAGAGCAGC      60
GGGAGCGGCG CGGGGAAGGG GGCAGTGTCC GCAGAGCAGG TGATTGCTGG CTTCACCCGC      120
CTTCGGCAGG AACAGCGAGG CCTGGCATCC AAAGCAGCTG AGTTGGAGAT GGAGTTGAAT      180
GAGCACAGCC TAGTGATCGA TACACTGAAG GAGGTAGATG AAATCGTAA GTGCTACCGC      240
ATGGTTGGAG GAGTGCTGGT GGAGCGAACT GTCAAAGAGG TGCTGCCCGC TTGGAGAAC      300
AACAAGGAGC AGATACAGAA GATCATTGAG AACTGACAC AAGCAACTCG AG              352

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GAATTCGGCC AAAGAGGCCT AGCTAGGTTT TGAAGCTTCT GAGTTCTGCA GCCTCACCTC      60
TGAGAAAACC TCTTTGCCAC CAATACCATG AAGCTCTGCG TGACTGTCTT GTCTCTCTCTC      120
GTGCTAGTAG CTGCCTTCTG CTCTCTAGCA CTCTCAGCAC CAATGGGGTC AGTCCCCCCC      180
CCCGTACACG CCTCGAGGCA GGTCCGAG              207

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

GAATTCGGCC TTCATGGCCT AGGCGGGACT AACACAGGCT TGTATCTTT TCCTTTTGCC      60
AAGAAAGAAC ATTAATAATGT ACTACCAGCA TCTGCCATCA CTAGCATTTT ATAAAAAGAG      120
GTTCTGTTAG CAACAGAGTA GAACTGTAG GAAAGCATCT CAGAACAAAA CTAAGTTGAA      180
TAAATTCACC TAATAAAAT GCCTTGGTCT AGGATTTCCT TTCTTCATCA AAAGCTGCAA      240
GAGAAAGCCA CTGCTTACCT GATGCCGATT TACTGGTCAT TGGGGTGGGG AGGTTTGGTT      300
CTCGAG              306

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

GGTCTCACTT GTCTATCCT GTCGCCAGG CTGGAATGCA GTGGTATGAT CTCAGCTCAC      60
TGCAACCTCA GCCTCCTGGG TTCAAGTGAT TATCTGCCT CAGCCTCCAA GTANCTGGGA      120
CTATAAGCAC ACATCACCAC ACCCAGCCAA TTTTTTTGAA TTTTAAATAG GGTTCACCTA      180
TGTTGGCCAG GCTGTTGAA CTCCTATCCT CAAGCGATCC ACCCACCTCG GCCTCCCGAA      240

```

GTGCTGGGAT TACCTGAGCC ACCGTGCCCCA GCCCATTTC A CAGTACTTTT TATTTAACCC 300
 TATCGTGCTA GGGCACCATG CAATATACAG CTATTTCATT TTCCTTTTGT CTCTGTTTCT 360
 TAGGTGGTCT CGAG 374

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAATGGCAG GAATTCGAAA TATTGGCATA TGGTTCCTTT GGATTAGATT ATATAAAATC 60
 AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTCTCT GCATGATACT TCTGCTTATT 120
 GTCCTTCACA CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC 180
 CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT 240
 TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG 300
 CTCGAG 306

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTAGAGATA ACAAACAGG ATACCAAAGT TGAGCTGGAG ACTTACAAGC AAACCTCGGCA 60
 AGGTCTGGAT GAAATGTACA GTGATGTGTG GAAGCAGCTA AAAGAGGAGA AGAAAGTCCG 120
 GTTGGAAGTG GAAAAAGAAC TGGAGTTACA AATTGGAATG AAAACCGAAA TGGAAATTGC 180
 AATGAAGTTA CTGGAAAAGG ACACCCACGA GAAGCAGGAC AACTAGTTG CCCTCCGCCA 240
 GCAGCTGCAA GAAGTCAAAG CGATTAAATT ACAGATGTTT CACAAAGCTC AGAATGCAGA 300
 GAGCAGTTTG CAGCAGAAGA ATGAAGCCAT CAGCTCGAG 340

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCGGCC AAAGAGGCCT AGATTTTAAA TTGTTTGAT ACCTGCTGTG TATTCCTTGC 60
 ATACCCAGCA CATTGTTGCC CATATTGTTG ACATGTAGTA TGTATTTATT ACAATTATAT 120
 GATTAATGAA ATGTATCTTA TTTTTCAT GTATAGCATG TACAGTCACA CTCGAG 176

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

GAATTCGGCC AAAGAGGCCT ATTCTTTGTC TTTTGACAT GTTCTTTGAG TCTTAGTATC      60
TGTAACGTGG CGCTACTCTC TCTATCATGG GGGGGCATGT TTTGACATTA AATTGACTTT      120
TAAGAAAAAC ATGTCATAA CCTGAAGCTC AGCCACACAG TGACTTTTAA GGTTTTATTT      180
AGACTTTACT GTTGTCTCA TGAGAGTAGG TACAGACTGC ATAAGGTTTA GAATCCCAGC      240
ATATGTCTGA AACGACGGGA CTTTCACTGT GATTTCCACC AGAGAAATTA TAGCAGAGTG      300
GCTGAGCATG TGCTCTGAGG CCAGGCCCA GCTCTGCTGC TGACGAGCTG TGTGGTCCTG      360
GGCAGAGTGG TCTCCGAGTT CCAGTCCTC CTCTGTAAAA TGGGCTTACT CGAG              414

```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

GAATTCGGCC AAAGAGGCCT AAACATATAC CTAGTCTATA CTCTCTCTTA TCTCTGAACA      60
CTTTTCATCT GGAGCTATTA ATGCCCTCTA GCCTTTATTA TAATTATCAC ATATAATTAT      120
GCCTTTTCTC CTCAAAATTA TCTGTTGGAG TCATCTTATA GTAGAGTCTT TACAGAACAC      180
AAAGCATTCA ATCACTTTAT TTCAGACACC AACCTTGTTT TTGATGAACA TATGTTAGTC      240
TTAAGCCATC TAAAGTAATG CTAATGTGGG ATCTTATGGA AGACTACTGG TAATACAGGA      300
AAAAAAGTGG CAAAGAAATC TGACACGTTT GGCAATTATT CCTGAGGCTC TGACCTCTCA      360
ATTGTTGAGT GTTGGAGGTC ACAGTAAACA AACCATATAA AGATCATGTT GAAAGTCAAC      420
ATTATTAATA TACCATACTT GAAGGATATG TGGTTATTGT CTCACGTGTC CATGTGAAGA      480
GACCACCGTC CCTCGAG              497

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

GAATTCGGCC AAAGAGGCCT AGTTTTTGAT GAATTTGTGT TATTTACTTA TAACTAGAGT      60
TTGAATGTTT ATTGGGAAAA CTTAATCATG ATCATCTACT GGTGGCTCGA G              111

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCGGCC AAAGAGGCCT ATGCAATTCT GACCAGGAAG CTCCTCTTTA ATTGGAAATT	60
CTTAGAAAGG TATGGAGCAA AGGAGATCCC AGCAAACATT CCGGCATCTA CTGCTCTTGG	120
GTTTTTCTG TGTTGGTTTT TTTTGTCTTG TTTTGTCTAT GAGATGGAGT CTCACTCTGT	180
CGCCCAGGCT GGAGTGCAGT GCGCAATCT CAGCTCACTG CAATCTCCAC CTCCAGAGTT	240
CAAGTGAATA TCCTGCCTCA GCCTCTCAAA CAGCTGGAAT TACAGGTATA CACCACCACA	300
CCGAGCTCGA G	311

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCGGCC AAAGAGGCCT AAGTGCAGTG GTGCGATTAT AGCTCACTGT AGCCTCAGAA	60
TCCTGGGCTC AAGCTGTCCT CCCACTTAGC CTCCCAAAGT GCTGGGACTA CAGGCGTGTG	120
CCACGGGGCC CAGCCATTTT TCGAATATT TTCAATCTGC AGTTGTTTGA ATCCACAGAT	180
GCAGAACCCA TTTCTAATGG AGGGCTGACT ATACCTTTCT GATGACCTAA ATATTTGTGT	240
CCACTATTGG GACACTCCTT TCTTAGTGTC AAGGTTTGTG AGAAATTGAG GGCTGTTTGA	300
TGGGCAAAGA TTTATTATT TATTTACTGG CTTATCTACA ATTGAGACAG GGTCTCACTA	360
TGTTTCTCAG GCTAGTTCTA ACTCCTGGGC TGAAGCAGTC CTCCCATCTC AGCCTCCCAG	420
AGTGCTGGGA TTACAGTGT GACACCAT ACCCGGCAGA GCAAAGAGTT AAGAGTACAA	480
GACATTGAT CATCTGAGG AGTATTACT TCAGACTGAA ACACCACATG AAATTTCTAGA	540
GTCCACAGA AAGTGAATA ATTTTGTCT TTTCCCTTCT TCCGCTACAT CCTCGAG	597

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCGGCC AAAGAGGCCT AATTCTAGAC ATGCTCAGCT TTGTGGATAC GCGGACTTTG	60
TTGCTGCTTG CAGTAACCTT ATGCCTAGCA ACATGCCAAT CTTTACAAGA GGAACTGTGA	120
AGAAAGGGCC CAGCCGGAGA TAGAGGACCA CGTGGAGAAA GGGGTCCACC AGGCCCCCA	180
GGCAGAGATG GTGAAGATGG TCCCACAGGC CCTCCTGGTC CACCTGGTCC TCCTGGCCCC	240
CTGGTCTCGG TGGAACCTT GCTGCTCAGT ATGATGAAA AGGAGTTGGA CTTGGCCCTG	300
GACCAATGGG CTTAATGGGA CCTAGAGGCC CACCTGGTGC AGCTGGAGCC CCAGGCCCTC	360
AAGGTTTCCA AGGACCTGCT GGTGAGCCTG GTGAACCTGG TCAAACCTGGT CCTGCAGGTG	420
GTGCTGGTCC AGCTGGCCCT CCTGGCAAGG CTGGTGAAGA TGGTCACCCT GGAAAACCCG	480
GACGACCTGG TGAGAGAGGC CTCGAG	506

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GAATTCGGCC AAAGAGGCCT AGTCTGTGGT CATTTC AAC TCTCATTAT AGGATTCTAA      60
AAGGGCACTA CATTACTCCA CTCCTTATC TAAATAAAT TTAAAATTCA TCGGAATTG      120
TCCAGTCCTC CATCACTGGA AAATGTACAG ATTCTTCTC TGGAAATATC TAAAGAAAAG      180
TACAGCTAAT GTTCCCCCAT TTCGTGTTGT TTTGTGCTG CTTTAACTAT GAACTCATCT      240
GGCCGGGCGC AGTGACCAAG CCGCCGGGAG CTGGGGAGAG ACGCACCGGG GCGGCGACTG      300
GGCCAGGAGA CCAGAACACT CGAG                                         324

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

GAATTCGGCC AAAGAGGCCT AGGAGCAGAT TCCTCATGGT GCTTGTTTAT TATATATATT      60
TAATCCTGCT TGACACTTTA CCAAGGGAG ATGGTCCCTT TTATCAGTTG AATGTTAGCA      120
GCGTTATTTT AGAGTGTGGT GACTGGTTAG AGAACTCAT GTACTCAACC AGCCACAGTT      180
TCAAACAAAA TTTTATGTG CAAAGGACAG CAACCTTCTT GTATGTTAAA CCACCAGTAC      240
TCGAG                                         245

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

GAATTCGGCC AAAGAGGCCT AGGTGCTTTG GTTTTGTGCT TTTTAGTCAT CCCCATGAGA      60
ATAATAAACT CCATGAGGGC AGCAACTTGG CTGGCCTGTG TGCCAGTGCT GGGGACATCA      120
CTGAGAAATG AAGGCCATT TGGCAGGCTA TTTTGTAGCA AGATTCCTGA GGCCCAATCG      180
TTGGGTGATG AGATGGACCC GAGGTATTTT ACTCCAGCTC TCGAG                                         225

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCCAAAGAGG	CCTAGAGAGC	TCTGGGGGGC	AACCTGGAGG	TCTGAAAAGA	GGAGCCAGAG	60
AAGGTGGTAC	CAGGCTTCCT	GGTCAGAACC	GGCCTGGAGC	TCCTTCCCTT	CCCCCTGGCC	120
TGAGAGGTG	CTTTAAGTC	TTCCACCCCT	TGTTCCATCT	GCCTGCCAAC	CCATCGGAAA	180
GGAAATCCACA	TCATATTGGA	GATGACCCCA	TCAACCCAG	GGCTCCAGCA	CTACCAAGTT	240
GGAAATCCAC	GCCCGGGAGT	GGGGTAGAGG	AAGACGAGAC	AGGACGAGGC	AGAAAAGCAC	300
ATTTTAAAAA	CCAGACAAGA	TGGCTAGGCC	ATCACCAACC	AACGGACTTA	CCTTACATTT	360
TTGTAGGTAA	TTCCCCCAA	ATCTTGATTT	TTTTTTTCCT	CAATTATCCT	TTAAAAATA	420
AGAAAACACA	TTCAAACCC	ACTCGAG				447

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGATTGAAT	TCTAGACCAT	GCCTGCTCTG	GGCCCAGCTC	TTCTCCAGGC	TCTCTGGGCC	60
GGGTGGGTCC	TCACCCTCCA	GCCCCTTCCA	CCAACTGCAT	TCACTCCCAA	TGGCAGGTAT	120
CTGCAGCAC	TGGCAAGGGA	CCCCACCTCA	GGCACCCTCT	ACCTGGGGGC	TACCAACTTC	180
CTGTTCCAGC	TGAGCCCTGG	GCTGCAGCTG	GAGGCCACAG	TGTCCACCGG	CCCTGTGCTA	240
GACAGCAGGG	ACTGCCTGCC	ACCTGTGATG	CCTGATGAGT	GCCCCCAGGC	CCAGCCTACC	300
AACAACCCGA	ATCAGCTGCT	CCTGGTGAGC	CCAGGGGCCC	TGGTGGTATG	CGGGAGCGTG	360
CACCAGGGGG	TCTGTGAACA	GCGCGCCTG	GGGCAGCTCG	AG		402

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCGGCC	AAAGAGGCCT	AGTGGAAGAT	TTGGGTACTG	TCTTTAATAA	ATCAATCAAT	60
CGACTCTTAT	TTCAAGGAGA	AAGTTCTATG	TTATATGTG	AAGGTGAACA	GATCATATTT	120
AGAGGATATA	ACAATTAGAA	ATCTAGAAAA	TAATTATCAC	TTTTATAAAA	TTTTTAGTCA	180
ACTGTACAAA	TAATTACATA	AAACATCAAT	TAATTATGCT	TAAAAATCAC	TAATGTTTAT	240
AATATATAAT	CATTATTTGT	AATCAAAAGT	TTAATTTTAT	GCCAAAAAAT	AAAAAATGCT	300
TACTCGA						307

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCC	AAAGAGGCCT	ACTTCCATAA	CCGTGCTTTT	GACGTAAAA	ATTTTAAATT	60
CAGCCTTTTG	GAGAACACTA	AGTATCTTAG	TGTGTTTTTA	CTTACTATAA	TAATATTATT	120
GACCTAGTGT	AATATTACTG	CCATATGGAC	CTCAAGGGTA	CTTTTCTGAT	AAATTCTGT	180
TATGGTTTCA	TAATTAAACA	AAAGGATAAT	ATACAGAGTT	GTGGAGTTTT	TTTGGTTTTG	240
TTTTGTTTTG	AGATAGCCTG	GGCAACGAGT	GAAACTCTGT	CACACACACA	CACACACACA	300
CACAGACACA	CACCAAATCT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGGCT	TCATGGCCTA	CAAGAAGATG	AAGAAGATTG	TGGATGCCGT	GATCAAGTAC	60
AAGGACAGCA	GTGGACGTCA	GCTCAGCGAG	GTCTTCATCC	AGCTGCCCTC	GCGAAAGGAG	120
CTGCCCCGAGT	ACTACGAGCT	CATCCGCAAG	CCCGTGGACT	TCAAGAAGAT	AAAGGAGCGC	180
ATTCGCAACC	ACAAGTACCG	CAGCCTCAAC	GACCTAGAGA	AGGACGTCAT	GCTCCTGTGC	240
CAGAACGCAC	AGACCTTCAA	CCTGGAGGGC	TCCCTGATCT	ATGAAGACTC	CATCGTCTTG	300
CAGTCGGTCT	TCACCAGCGT	GCGGCAGAAA	ATCGAGAAGG	AGGATGACAG	TGAAGGCGAG	360
GAGAGTGAGG	AGGAGGAAGA	GGGCGAGGAG	GAAGGCTCCG	AATCCGAATC	TCGGTCCAGT	420
CTCGAG						426

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCGGCC	TTCATGGCCA	ACACATAATC	CACGCTCATC	TGCAAAGCG	CTATTTCAGG	60
CACATCATTG	GAATACAGGA	AGTAGCCCTG	CACCTGCCAG	TGAGCTCGCC	ATTCAGTGAT	120
TGGAAGAGTG	ACCTGGCATC	TTGGAATCA	TTGTGTGTCT	TCAGGAGAAT	GTGCAGTGTC	180
TTGTAACAAAC	TAATTATAAT	GCAAATTAGG	GCTACATTGT	AATCTGCTTT	GTTAATGAAA	240
ATGATAAAAC	AGAATATTGA	CAAGCTAGGA	CACCTGTGGT	ATCTTTAATT	GTATCTCCTT	300
CAGAAGTTTG	CTTCTTATGG	TATAATAAAG	TATGGAAGAA	TATTGAGTAT	ATGTTTACTC	360
TGGGCCTGGG	AGAACTTAAC	TTTCTAGAGC	AGTTTGTGTA	CTTGTGTGCA	ATGGGGAGAG	420
GTACCATGAT	GACACTCACA	GGGAGCCACT	GTTCACTGAC	ACTTGAAGG	CCCTGCCTCG	480
AG						482

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GTGTTTGCCC ACACCCTCCT TGAATTTAAC TGCCACAATC TATCCGCAGA TGTGTTTTGT      60
TCTGTTTCTT GTTTTTCAC T AGCGTTTGCG TTGCTTCCTC TGAAGCCAGA GGGTGAAAAG      120
CCCTAGCAAA GTTAGTTATC AGTCAACTGA TGATAACTGT GATCCTTAAA GATGAATTCC      180
CAGCCTGAGG TGACACACAG AGGTTTCAGCA GACGTCTCAG GATCTGTCAC ATGTCATGTT      240
GCTTGGTGTG AAGATGGAAG AACAAAGTCC ACATCAGTTT CTGCTCCTTC AAACAGTGTG      300
TCGATATGAA ACATTGAGAT TTGGCAGAAA CATGTGCCTA GTTTCAGCA CCAAATACTC      360
GAG                                                                                   363

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(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

GAATTCGGCC TTCATGGCCT AAAGGGATAT TCACTCAAAT CCCTAAGTAT TTCAGAAACA      60
GCCTGAGAGC AAGTCCTTGG CTTGCTTTC TAGTTTTAAA AGGCTTTTAA CTGTTTAGTC      120
TGAGATTCCC CTAAAAGTTC CAGGAAAGCA AACTCAAAAA GAGCCTAGGT GGTCAATCAT      180
TATTTTGTCT GCGTTTATAT AAATAATCAG GCCAAGTTAA TGAGACTAAA CTTATTTTGC      240
AAGCAAATCA GTCTTTGCTT ATTTTGGTA GGAATGGGGG TAAATGGAGA GAGAGAAATT      300
ATGTTTCAGA AGAAACTAT AGCACACCAA CTCGAG                                                                                   336

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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GAATTCGGCC TTCATGGCCT AGTGGGAAAC ATTATTTCAA GACATTAGGG ATAAGAATGC      60
CAGTTGCTAC TGAGTTGGTT ATTGTTTCAA GGATTTATCA ATACATAGAG CAAATAATTA      120
TGTTTTGCTT TGTCTTATTT TTATTTCTTT ACTTTAGAAA CAGTACAGCT ACTTACAAAT      180
CAAGTTTAGA ACTCTCAGGT TATCTTAAAT CTGAAGCTTC TACCTTCCTA AGAACAAAAC      240
ACCGGCTCGA G                                                                                   251

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(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTTCACCAG	TTCAAATACT	TTTCAACCT	CTATTTCTTA	CTTCTTGCCT	GCTCTCAGTT	60
TGTTCCCGAA	ATGAGACTTG	GTGCACTCTA	TACCTACTGG	GTCCCCCTGG	GCTTCGTGCT	120
GGCCGTCCT	GTCAATCCGTG	AGGCGGTGGA	GGAGATCCGA	TGCTACGTGC	GGGACAAGGA	180
AGTCAACTCC	CAGGTCTACA	GCCGGCTCAC	AGCACGAGGC	ACAGTGAAGG	TGAAGAGTTC	240
TAACATCCAA	GTTGGAGCCC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCGGCC	TTCATGGCCT	AAGATGATTG	TGCTATTATT	GTTTGCCTTG	CTCTGGATGG	60
TGGAAGGAGT	CTTTTCCAG	CTTCACTACA	CGGTACAGGA	GGAGCAGGAA	CATGGCACTT	120
TGTTGGGGAA	TATCGCTGAA	GATCTGGGTC	TGGACATTAC	AAAACTTTCG	GCTCGCGGGT	180
TTCAGACGGT	GCCCAACTCA	AGGACCCCTT	ACTTAGACCT	CAACCTGGAG	ACAGGGGTGC	240
TGTACGTGAA	CGAGAAAATA	GACCGCGAAC	AAATCTGCAA	ACAGAGCCCC	TCCTGTGTCC	300
TGCACCTGGA	GGTCTTTCTG	GAGAACCCCC	TGGAGCTGTT	CCAGGTGGAG	ATCGAGGTGC	360
TGGACATTAA	TGACAACCCC	CCCTCTTTCC	CGGAGCCAGA	CCTGACGGTG	GAAATCTCTG	420
AGGGCGCCAC	ACTCGAG					437

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTCGGCC	TTCATGGCCT	AGTACCTTAA	AAACTTTGGA	AATAATAATA	ATAATAATAA	60
ACAAAAAATA	ATCCCAAACC	CGTAAGTTT	AACTTTCTAT	GCTTTGGCTG	TTTTTGTTT	120
ATTTTTTGTT	TTTLAGAAGG	GGTCTCGCTC	TGTCGCCCAG	AATGGAGTGC	AGTGGCTTAA	180
TCAGGGCTCA	TGACGCCTC	GACCTCCTTG	GTTGCGGCGA	TCCTCCTCCC	TCCCACTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AATTAAATTA AATTAAAATC TTTGTTACAA ACTATGAAAA TGAATATAAG TAAATTTCAT	60
ATCATTTCTT TTCTAGATTT ATTATCTAGG ATAGATTTGG ATGAACATAAT GAAAAAAGAT	120
GAACCGCCTC TTGATTTTCC TGATACCTG GAAGGATTG AATATGCTTT TAATGAAAAG	180
GGACAGTTAA GACACATAAA AACTGGGGAA CCATTTGTTT TTAACACCG GGAAGATTTA	240
CACAGATGGA ACCAGAAGCT CGAG	264

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCGGCC TTCATGGCCT AACCTGGAGA AACTATTTAA GTTGGATGAA GCAAGTGCCC	60
AGCTCCTTGC TTATAAGGAA AAAGGCCATT CTCAGAGTTC ACAATTTTCC TCTGATCAAG	120
AAATAGCTCA TCTGCTGCCT GAAAATGTGA GTGCGCTCCC AGCTACGGTG GCAGTTGCTT	180
CTCCACATAC CACCTCGGCT ACTCCAAAGC CCGCCACCCT TCTACCCACC AATGCTTCAG	240
TGACACCTTC TGGGACTTCC CAGCCACAGC TGGCCACCAC AGCTCCACCT GTAACCACTG	300
TCACCTTCTCA GCCTCCCAG ACCCTCATT CTACAGTTT TACACGGGT GCGGCTACAC	360
TCCAAGCAAT GGCTACAACA GCAGTTCTGA CTACCACCT TCAGGCACCA TAGTGACTCG	420
AG	422

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAATTCGGCC TTCATGGCCT ACCGAAGGGC ATCCCATCGG TTGGGTAGGT CATGGTTAAA	60
AAATCATCTC CTTTGTTGTC ATATTAAATT ATTTTCCACT ATTTTTCCT CACACAAAAT	120
GATTTTGCCC GGTACCCTTT TTGGGGGTGC ACAGTCCATG AGATGAATAT TGAATGGGGA	180
GACCTGGGTT CTAGTCTCGC ATTTACCACT CAGGTTACAA TGCGACCTTG AGCAAGTCAC	240
TTACCTCCC AGCGCTCAG TTTCTCATT GTAAGATAGG AAAAGCCTTG TCATTTTAA	300
AATTTTATTT TTTGCATATA CCTCATGGCG AACTCGAG	338

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCGGCC	TTCATGGCCT	ACTATGCTCT	GCACGTGGGT	CATTTCTTAC	TGGTTTCTAA	60
AAGCCTTTCA	TTTTCTGCCT	GTACACAATA	GCCCCCTTCC	TCCATTGTTT	TTAGGATCCT	120
TTTTCCTCTT	ACCAGCTGTT	AACCTGGAAG	TATTTCTTCT	TCATCCCGAA	TCTCCCATGT	180
CCTCCCCACT	TCTATTTGTT	TCCATCCAAT	GTGGATTCAT	GATCATTTTA	TGGATTTTAA	240
ACTACTCTGG	GGCTACCCTC	GAG				263

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCGGCC	TTCATGGCCT	AGAAACACAT	GTGATCTGTA	CTCATGAGAA	CCTGTAGTTA	60
ACTATACGAG	CCTTGCTGTG	CATTTTGTTT	TTATCTGAGC	CTGTCTTTCA	ATGTCCTATC	120
CCTTGAGAGA	ACTGAGGGCT	GAGAACCAAG	CTTTCCGAAG	CGGTCTGAGT	GTCAGCGGTG	180
GTAGTGGTCT	CTGGAGAAAA	GAATGGAGAC	AGGATAGGAC	TTGGAGAAGA	GTGAGTCATT	240
GTTACCCAGA	AACCCTGGAG	AACACTGGAC	TCGAG			275

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGCGTTCTC	ACGCCCGCAA	CAATTCCTGA	GTAGGGCCTT	GCTTGAGTTC	TTCGGAAAGT	60
CTCATCCACC	CCCACATCGC	CTCTTTAGGA	AGTCACTTAA	TGTTGGGCTT	CATTATTCCC	120
ACATCCCTTT	CCTTACTACT	TGCCTGCACT	TCTTGAGAAA	AAGACTGCAG	AAAGGAGAGG	180
TGGGGCTTTC	AGTAGAAACA	AGCAAACCGC	AGGTCCCTGT	GGGGGGACTC	TCCAGGAAGA	240
AGGGTAATTT	CCTGCCTCCT	TAAATTGGCT	GCTACTGTCA	GTTATTTTGC	TCCCAACCCC	300
AGAGCTTCAC	TTGCTCCTTC	ACTTCCCAGT	TCCGCAAGAA	CCGTGGGCGA	CAGTTATGGA	360
GAAGCGTCTG	CAGGAGGCTC	AGCTGTACAA	GGAGGAAGGG	AACCAGCGCT	ACCGGGAAGG	420
GAAGTACCGA	GATGCTGTGA	GTAGGTACCA	TCGAGCTCTG	CTTCAGCTGC	GGGGTCTGGA	480
TCCGAGTCTG	CCCTCTCCGT	TACCTAATCT	CGGACCTCAG	GGCCCGGCCC	TCACGCCTGA	540
ACGACCTGCC	TCGAG					555

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

GTGAAGATGG ACTGCTCTGG GGCCCATGTG CAAGTGACCT GTGCCAAGCT CATCTCCAGG      60
ACAGGCCACC TGATGAAGCT TCTCAGTGGG CAGCAGGAAG TAAAGGCATC CAAGATAGAA      120
TGGGATACGG ACCAATGGAA GATTGAGAAC TACATTAATG AGAGCACAGA AGCCGAGAGT      180
GAACAGAAAG AGAAGTCGCT TGAGCTCAAA AAAGAAGTTC CAGGATATGG CTATACTGAC      240
AAACTCATCT TGGCATTAAT TGTTACTGGA ATACTAACGA TTTTGATTAT ACTTTTCTGC      300
CTCATGTGA TATGTTGTCA CCGAAGGTCA TTACAAGAAG ATGAAGAAGG ATCACTCGAG      360

```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

GAATTCGGCC TTCATGGCCT AGCTCCTGCG TAAAGGAGCA TGAGAGCGTG GGAGTTTTC      60
AGTGGCCGTG GGGTTCTTCG TCGCGTCTCG GTCGGGCGTC GCTTTCTGCA GCTCCTGTCA      120
GGGAGCGCGA GGCCTGTTAT TAACCGCGGA GCGCTTTGTC ACGAANTCCC TGTGGCGTCT      180
TGAAGAAGGC ATTCCCCACC CGCCAAATGG CGTCCATGCC CCCGACGCCC GAGGCCCAGG      240
AGAGTCGAGG TACCTTTTTC GTCCAAGTTT ATNGCTGCTT TCGGTCTCTG CCTGACCCCN      300
TCCTTTGGAG GAGAGTTGGG CATGCCTGTT GTGGTAGGAG TGCTCNTGAG CCCCAAATAG      360
CCCTTTGACC AAGTGTTCCT CGTTCCAAGA CCACACACAT AATGGTTTAC CAACTTCNTT      420
CTTTCAGAAC TACCAACTGG GAGCAGGGAC CTGTGGAGGA ATCTCTGAGA GAGTTTCTCA      480
ATGTCTTATC TGTTTGTTTT GTTTTGTTTG GAGATAGGGT CTGGCCTTGT CGCTGGAGTG      540
TTGCTTGTCT GGCTGGAGTG CAGTGCTGAT ATCATAGCTC CGTCTGGAAC TCAGGGAATC      600
CTTACGCCTC AGCCTCTCGA G                                     621

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

GAATTCGGCC TTCATGGCCT ACAATTTGGA GCAAGGCTTA GCAGAAGACG GCGGCATGAG      60
CAGCGTGACT CAGGAGGGCA GACAAGCCTC TATCCGGCTG TGGAGGTACG GTCTGGGCCG      120
GGTGATGTAC TCCATGGCAA ACTGTCTGCT CCTGATGAAG GATTATGTGC TGGCCGTGGA      180
GGCGTATCAT TCGGTTATCA AGTATTACCC AGAGCAAGAG CCCAGCTGCG TCAGCGGCAT      240
CGGCCGGATT TCCCTGCAGA TTGGAGACAT AAAAACAGCT GAAAAGTATT TTCAAGACGT      300
TGAGAAAGTA ACACAGAAAT TAGACGGACC TCTCGAG                                     337

```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCGGCC AAAGAGGCCT ACATTACTGG GTTAGAAAAC AAAGAGGGAG TGCCCTGCAC	60
ATTTTCTTTT GTGCTTTTAA ATGTTTCTTA AGTTGGAACA GGTTCCTCG GGCCTGTTTT	120
GACTGATTGC TGGAGTGCAT TTGATAGTTA AAAATTACTA ATTGGTTTTA TTTCCCTTCA	180
CACTCTGCCT CCCCTATTTC CCCCAATTGA CCCTAAACCT CGAG	224

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATTTAATGC ATGCTAGCAA CAGCCTTAAC TTTGGATTCA GTTATTGAA ACACTTTTCC	60
GGCATCTTTC CCTTTCTAAT GTTGTGGGGT GGAAACCGGA TGGCAAATCA CTGTGAGCCG	120
GATACCTCAG CACAGTCCAC CTTGTGTGTG ACTTCACAAA TGGGGGACTT CACAAATGGG	180
GTAAGTGAAT GTTATTACTT TCAAATTTG ACATGGAGCA TTATGATCAA GGAAATGGAG	240
CAACTCGAG	249

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCTGCGCCGC ACCCTGAGAG ATGTTTGGTG CCATGTGGAA GGTGATTGTT TCGCTGGTCC	60
TGTTGATGCC TGGCCCCTGT GATGGGCTGT TTCACTCCCT ATACAGAAGT GTTTCCATGC	120
CACCTAAGGG AGACTCAGGA CAGCCATTAT TTCTACCCC TTACATTGAA GCTGGGAAGA	180
TCCAAAAAGG AAGAGAATTG AGTTTGGTCG GTCCTTTCCC AGGACTGAAC ATGAAGAGTT	240
ATGCCGGCTA CCTCGAG	257

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

GAATTCTAGA CTTTGTCTCC AGAGCATTGC CTTTATAAGC AGATTGGCAC CAACAGTTCC      60
ATAGTTTAAAC ATCTAGTTAA GCTACAAATA TAGTATAAGC ATTATTAGCA GCTGGTACTT      120
CTGCTAGGGG TTGTAAATTC CAGGTGTTAC ACTGACCTCA ATCCAATTTA CATAATTTAC      180
ATAAATGCAT CTCGGTGGAA AAATAATCAT TTTCTTGGCA TATCTCGAG      229

```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

GAATTCGGCC TTCATGGCCT ACACTGCTAT GTATGTTTTC TCCTTAATGA TGAAGAGTGT      60
AGATGATGCT AATAATAGTA GCTGATGTAC TGACTTTTAG CTGTGTGCAA AGCCATGTTT      120
AAAATACTTT ACAAGTGTTA ACTTGTTTGA TCTTCACAAC AACCCTAAGA AGTGGATATT      180
ATTAAAGTAG ATTTTGGAAG ACTGATCTAT TTAATTATTA ATAGATCTGT CTCATTCCTT      240
TTTTCCCCCA ACTCGAG      257

```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

GAATTCGGCC TTCATGGCCT ACGCGTCTGC TTCGGAGACC GTAAGGATAT TGATGACCAT      60
GAGATCCCTG CTCAGAACCC CCTTCCTGTG TGGCCTGCTC TGGGCCTTTT GTGCCCCAGG      120
CGCCAGGGCC TTTGTGCCC CAGGCGCCAG GGCTGAGGAG CCTGCAGCCA GCTTCTCCCA      180
ACCGGGCAGC ATGGGCCTGG ATAAGAACAC AGTATCACTC GAG      223

```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

GAATTCTAGA CCTGCATGTC CCAGTGTGAA ATTTCAGCAC GGCATTTTCT GCATCCTTTC      60
ATGGCCATCC AAAGGATTCC GCTGCAGAAA TTATTGATGT GCTATTTTGT CTGTCTTGTG      120
ATGCAGGCTG CTTTGGGCCC CTGGGTCACT CTTCGAAGGC TGCAACTCGA G      171

```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

GAATTCGGCC TTCATGGCCT AAAAAGCAAA AGAAAAGTAA AAGGAAGAAA CAAGAACAAG      60
AAAAAAGATT ATATTGATT TAAATCATG CAAAACTGC AACTCTGTGT TTATATTTAC      120
CTGTTTATGC TGATTGTTGC TGGTCCAGTG GATCTAAATG AGAACAGTGA GCAAAAAGAA      180
AATGTGGAAA AAGAGGGGCT GTGTAATGCA TGTACTTGA GACAAAACAC TAAATCTTCA      240
AGAATAGAAG CCATTAAGAT ACAAATCCTC AGTAACTTC GTCTGGAAAC AGCTCCTAAC      300
ATCAGCAAAG ATGTTATAAG ACAACTTTTA CTCGAG      336

```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

GAATTCGGCC AAAGAGGCCT AGAAGAGCAA GCGCCATGTT GAAGCCATCA TTACCATTCA      60
CATCCCTCTT ATTCCTGCAG CTGCCCCTGC TGGGAGTGGG GCTGAACACG ACAATTCTGA      120
CGCCCAATGG GAATGAAGAC ACCACAGCTG ATTTCTTCCT GACCACTATG CCCACTGACT      180
CCCTCAGTGT TTCCACTCTG CACGCTCTCG AG      212

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

GAATTCGGCC TTCATGGTCT ATGCTACTCA GTTGGATCTA GCAGAAACAA AAGCTGAGTC      60
TGAGCAGTTG GCGCGAGGCC TTCTGGAAGA ACAGTATTTT GAATTGACGC AAGAAAGCAA      120
GAAAGCTGCT TCAAGAAATA GACAAGAGAT TACAGATAAA GATCACACTG TTAGTCGGCT      180
TGAAGAAGCA AACAGCATGC TAACCAAAGA TATTGAAATA TTAAGAAGAG AGAATGAAGA      240
GCTAACAGAG AAAATGAAGA AGGCAGAGGA AGAATATAAA CTGGAGAAGG AGGAGGAGAT      300
CAGTAATCTT AAGGCTGCCT TTGAAAGAA TATCAACACT AACTCGAG      349

```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCGGGCTAGT	CATGGCGTCC	CCGTCTCGGA	GACTGCAGAC	TAAACCAGTC	ATTACTTGTT	60
TCAAGAGCGT	TCTGCTAATC	TACACTTTTA	TTTCTGGATC	ACTGGCGTTA	TCCTTCTTGC	120
AGTTGGCATT	TGGGGCAAGG	TGAGCCTGGA	GAATTACTTT	TCTCTTTTAA	ATGAGAAGGC	180
CACCAATGTC	CCCTTCGTGC	TCATTGCTAC	TGGTACCGTC	ATTATTTCTT	TGGGCACCTT	240
TGGTTGTTT	GCTACCTGCC	GAGCTTCTGC	ATGGATGCTA	AAACTGTATG	CAATGTTTCT	300
GACTCTCGTT	TTTTTGGTCG	AACTGGTCGC	TGCCATCGTA	GGATTTGTTT	TCAGACATGA	360
GATTAAAGAAC	AGCTTTAAGA	ATAATCTCGA	G			391

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAATTCGGCC	TTTCATGGCCT	AGGGAGTCTG	AAGCAATTTC	TGAAGAAGAC	CAAAAAGAAC	60
CACAAGACGA	TGAATGAAAA	GGCATGGAAG	CGTTGGTGCA	CACAAATCCT	CTCTGCCCTA	120
AGCTACCTGC	ACTCCTGTGA	CCCCCCCATC	ATCCATGGGA	ACCTGACCTG	TGACACCATC	180
TTCATCCAGC	ACAACGGACT	CATCAAGATT	GGCTCTGTGG	CTCCTGACAC	TATCAACAAT	240
CATGTGAAGA	CTTGTCGAGA	AGAGCAGAAG	AATCTACACT	TCTTTGCACC	AGAGTATGGA	300
GAAGTCACTA	ATGTGACAAAC	AGCAGTGGAC	ATCTACTCCT	TTGGCATGTG	TGCACTGGAG	360
ATGGCAGTGC	TGGAGATTCA	GGGCAATGGA	GAGTCCTCAT	ATGTGCCACA	GGAAGCCATC	420
AGCAGTGCCA	TCCAGCTTCT	AGAAGACCCA	TTACAGAGGG	AGTTCATTCA	AAAGTGCCTG	480
C						481

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATTCGGCC	AAAGAGGCCT	ACGATTGAAT	TCTAGATCTG	CCCGTCTTGG	CCTCGCAAAG	60
TGCTGGGATT	ACAGGCGTGA	ACCACTGTGC	CTGGCATATT	TGTCTATTAA	TTTGCTTTTC	120
TTTAGATGTA	TTCTAGAGGG	GGGAAAATCA	GTAGAAGAAC	AGTTATGTAA	TTCTAACCAAG	180
TTCTCCATGT	GTCTTGCCAT	CTNGCTTTTT	CTCATCCTAT	CAGTACTGGA	TGAGAATGTT	240
TATTTCACTG	AACCTTGCCA	AAGAGTTTCA	ACATTTTTTT	GTTTAATCAT	AGGAGAAAAA	300
GGTTTATCTT	ATTTTAAAAA	ATTTTATTTT	AATTCTTTCA	TTACAAATGA	AGTCCCAGAA	360
GTTGTATTTG	TTTCTTTAGG	CTGTTCTTAA	TTGTTTCATTG	GAACAGGCAG	GGTTTGAAGG	420
AGTGGGGATA	CTGGGAAAGC	CAGGCTGATG	AGAAAATAGG	AAAGGGGTCT	TGTCATTGGG	480
AGGCCACTAT	ACCACTGGCC	CTTGTAACAG	GACTAATATG	GTACTTTGAA	GCTTTAAATT	540
CATTCTTTTA	TTCAATAATT	TTAGGCATCC	CAGGATACTC	GAG		583

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

GAATTCGGCC AAAGAGGCCT AGCTATCCGC TTTGCTATTT TAGTGGCATT ATCAAAATCA      60
CTGGAAGCAC CTGTNGTAAT ATGGTCGGTT CCAAATATAA GTCCTCTGC CACTCTTCCT      120
CCCATACTAA CATCCATTG TGCAAGCAGC TGGGCTCTAG TTTCATTCCA TCTGTCATTC      180
TCAGGTAACA GGGACACATG TCCAAGTGTG GGCCCCCGTG GCATGATTGT AGCTTTGTTG      240
ATAGGCATTG CATCTTTTGT GTAATATGCA ATAATGGCAT GACCAGATTC ATGATATGCT      300
GTGATGGTTT TGTTTTGTG ATCAATTTC ACACCTCTTC TTTCAGGCCC CATTAGAATT      360
TTGTCTTTGG AAAACTCCAG CTCCTTCATG GTAACCATTT CTTTCCATC AACAGCTGCT      420
TTTAATGCAG CCTGGTTCAC AAGATTCTCC AACTCTGCTC CGGAAAAGCC AACAGTACCT      480
CGAG

```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

GAATTCGGCC AAAGAGCCTA ATTGAATTCT AGACCGGCCT CATCGTTCTT TGCCTTCCTG      60
GTCACCATCT GCTACGCTGG AAATACATAT TTCAGTTTTA TAGCATGGAG ATCCAGGACC      120
ATACAGTGAT TTACCATTTT GATAATTAAA AGGAAAAAAA AAGGAAGACT CTCAGTGTA      180
AAACAGCTGT AGGTATAATG TATATTCCCA GAGAATTGTA TTAACTAAT TAATGTTT      240
TATATTCTTA AATTGCTCA CAAATTGTGG TTTGTTACAA TTAAGTGA TACTTATTG      300
CAAAGTGTG TAGCTTATAA TGAAGTCTTA AGTATCTTAT TAATGTATTA ATGTCTTCAT      360
AGATCATATT TTCTTAGACA ATGTTTAAAT AGATAAATG CTAATATTGA GAATGTGTCA      420
AGTTTGTAAG CCTAACTTTT AAGATGCCAG AACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

GAATTCGGCC AAAGAGGCCT ACGGCCAAG AGGCCTAGGT GGTGATTGAC CTAAGAAAAA      60
AGTGTCTTAA ATATCTGGAT TCTATGGGAC AAAAGGGCCA CAGGATCTGT GAGATTCTCC      120
TTCAGTATTT ACAGGATGAA AGTAAGAACC GCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

GAATTCGGCC AAAGAGGCCT AGTGGACTGC TACTTCCCTT TAGCACTATA TACAAACATA      60
ACTGCTACTT CCCTTTAGCC CAGGATCAAA ATAATGATTC AGTTAAAAGT TGCTTGCCTA      120
ACAAAATTTC AAAATATGGA CTTCTGTGAA TTGCTAAAAC ACATCCTTTT AACTAGGCAT      180
CTTTAAGTCT ATAGTATCTT TAAAGTTAAT TTCAAAATTT AGCAGAGCCT GGAACACAAA      240
TTATTCAGGA AATAATTCCT GAACCTACCT CTATCTTCAT AAAACGTATT GGGGCAAGAA      300
CTATTCTATT GAATTCTAGA CCTGACTCGA G                                     331

```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

GAATTCGGCC AAAGAGGCCT ACCATCTGTC ACTAATATCA AAGGAGGGCC AAGGACACAG      60
CCCTGGGGGA ACTTACCAGG TCAACCCACA ATGGGTGAAT TTATAGTTTG TTAGTTAGTG      120
GTCAGTTACC AACTTCTCTG TCTGTCTAAT GCTTTGACTA AAATGTCCAG ATTATTTACC      180
TAGTTAACAA AATTAAAGAA GATTCTAAGA CCAGTTTAGC ATCATTITCT CTGAAGTCCA      240
TAATGAATGT CTGTAAACT CTCGTCACTC TTATTTAGGT GCTTTTGGGT CATTTTGTGT      300
AGGTTTATTC TCCCAAATCA ATGTCACATA TACGTCTGTA ACTTGTGTTA TCAGCTTCCT      360
TCCTAGGGCT TTAACITCTT TTCAGTCTTA TAGCATTCTT TCCATTTTCC TTTCAGTTCA      420
CTCCAATAAA AGCTCGACAA ACTCCTGGGA GCCCCTTGGT GCTCGAG                    467

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

GAATTCGGCC AAAGAGGCCT ACGATTGAAG TCTAGATGCA CACATTCAGC TTCTGTCTCA      60
GTCCTGAGAG TGGTTGTGTT TTATTGGCTG ATGAGTTATT TCCACATATC ACATGTATAA      120
GGTATTTGAA TGAAGGTGCT TTGTAGTCAT GACACACTAC TCTTTTACTA ATTATTAATA      180
TCTTAAGATT ACAATTTGAG AGGTAGAGAT GGTATTGTTT TTAATGGGTG TGGGGGGTGG      240
TGATGATAGG TATTTTACC CTGGTAAGTG ACCTACTAGG TTTTATTAAG TGTGCAACT      300
TGTCCAGTGT GTGGATGGGA TCTCGAG                                     327

```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

GAATTCGGCC AAAGAGGCCT AGTGGTGGTA TGTATTTGAG TTCACAGTAT TTGTTTATA      60
GCAGTTTTCG AAGCACATAC TGTGCCACGG ATTTCCAC ATTATTTTA GACAAGGGAA      120
CACAGCCATC AAAACTGATA CCATGGCCGG GCGTGGTGGT GGGTGCCTGT AGTCCAGCT      180
ACTTGGGAAC TCGGACATT CTCGAG      206

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

GAATTCGGCC AAAGAGGCCT CCACCATGCC CGGCCTCAAC GATATTGATT CTTGGGCTG      60
TAGTCAGTAT TGGATTATGA TCAATATTAT CACCATTAT TTTGTTGCTC CAGTCTCTCC      120
AGCTGTGGCC AATCCTTCAG TTGGATTCTT GTGCCCCATC AACATTCTCC ATCCTTCTCT      180
CGAG      184

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

GAATTCGGCC AAAGAGGCCG ACTTTATTAT ACCATACATA CTATAGGTAC CTGGGCACAA      60
GATAGGTCAG GGGGTACTGT ACCCTATTT ACATGCTTAA TCACATCATA AGGTTGCAGG      120
TGGTACTTGA AATCATCACT AATGAGACAG CAAATATGTT AGACTTGCTG GCCCAGCAAG      180
CCACAGAAAT AAGGATCACC ATCTATTAGA ATAGACTGGC TTCAAACTCG AG      232

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

GAATTCGGCC AAAGAGCCTA CTAAATTCCT TTGTTTGTG TTTTAATAT TCCATCGTTG      60
ATAGTTAATA TTCTTTTNGA GGTTTTGTG TAGACAAAGT AATGTTTTTC TGAAATGATT      120
CTAAGACAAT TGGTCAGAAA TAGTCTCTGC TTGTTTGGTT TATGTTTGGT CAGTTGTGCT      180
TTGATTATAG ATGGTTCCTC ATCTGAGATT AAAGTGGGAC AGAACTTCAA AAGTAAAGG      240
GTAAATGTTT GCTGTGATGC TTATGTGGCA CATGTGCTAG TCCTTGATAG TGGCGAGAAA      300
GATCTTAATT GCTCAAAGGA AGTACTCGAG                                     330

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

GAATTCGGCC AAAGAGGCCT ACAGTGCATT ATGTTATTTT GTTATCTCTG CAGTAACTTT      60
CTATCATGTT ATTTATTTTC TTTGTCTTAT TTAAAGCTTC TGAGATTATG GATTTTGTGTT      120
TCCTTCCCTG AAGTTAAGTG TTATCATTCC TATATAGTAC TAAGCTGTCT ACAGAATAGT      180
GGGAGTCTGC CCTCTTGAGT TGGGAAGATC CTAGTTTGAA TCTTGGCTGT GCGACTTTAA      240
AGTTCATTAA CTCTCTTAG CCTCAGTCAC CTGAACTCTG CAGTGGGGAT CCTTATGCCT      300
CAGAGTGTTA TTGGGAGGAC TCACGAAAAT ACGCTTGTA TTTGAGTTCA GTACCTAGCC      360
TGTATGAGCC AGCATTAAAG GGGACAGTCA TCACGCAGCG CTTTGCACAC AGCTCTCAG      420
CCACATCCTT TGGCTACTGT TTTGTTAAAT CTTTACTAGT AAATGTTTCT TAAAGCATT      480
TACATTCATG GACATGATTC CCTCGAG                                     507

```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

GAATTCGGCC AAAGAGGCCT AGATTGAATC TAACCTTTTT GCCTCTTCCC AAGTAGCCTA      60
TTTGAGCTAG AACAAAACCT TGTTAGCCAT TTTGGGAGAG AATAGGGAAT CTAGAGAATG      120
AAGATCTGCC CGACCTGCCT CGAG                                     144

```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTCGGCC AAAGAGGCCT AACGACGGTA ATCAAGTTT GCTCCAGAAG CATCAAGAAA	60
CTTAGCTACT GCTTCCAAAT CAGTACCGGT TTCAGTTAAG CCTTGAATAA TACAGTCTTG	120
AAACTGAGTA GGGTCAAACC TCTCTTTTTC ATCTCTTTT CTAGTTTAA AACGCTGGCC	180
TGATAGCGTT GGCTTTTGCT GCTTTTGATT ATTCATAAAA GACACCCGAA TTTAAGGCGA	240
AGAGGAAAGA GCCAGAAATC CCCGATGTAC CGGCAACTGC GGCGCTATCT CCTCGAG	257

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAATTCGGCC AAAGAGGCCT AGACTGCTGG TGGTGAAC TGCTTTCTGT AGGTTGTGAG	60
GGCTGAAAAA GCCAATCTTA ATAGACATGA GGTCATGTT TGCACAGTGT GCTCTCGAG	119

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAATTCGGCC AAAGAGGCCT ACTCAGCTGC AAAAAAGCAT ATTTTCTGTG TTTCTGGACT	60
GCACTGTNGT CCTTGCCCTC ACATAGACAC TCAGACACCC TCACAAACAC AGTAGTCTAT	120
AGTTAGGATT AAAATAGGAT CTGAACATTC AAAAGAAAGC TTTGGAAAAA AAGAGCTGGC	180
TGGCCTAAAA ACCTAAATAT ATGATGAAGA TTGTAGGACT GTCTTCCCAA GCCCCATGTT	240
CATGGTGGGG CAATGGTTAT TTGGTTATTT TACTCAATTG GTTACTCTCA TTTGAAATGA	300
GGGAGGGACA TACAGAACTC GAG	323

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCGGCC AAAGAGGCCT AGGCAAATCA GAACTCTTAA GTTGTTTCAT CCTTATTTTA	60
TTCTTAAAT AAAGAATTTC ATTTCAAATA CGGATTAATT TTTTCTCGG GAAAAACAC	120
ACTGTAAAC ATAATTTTCT ACCTTTTAAA ACGTTTACA ATTTATCCCA TCTTCTAACA	180
AGTTATGATA CTCATACCTG CCGAGGTTTC TCTAAATTG TCGCTGGTCT TCTTTTTCCT	240

CCATTTCCAA GGCTTAAAGA TTTTACCAAT GGTGGATAGT TTCCCTTTTC TTTTGAAGGG 300
 AGGTGTTTGG GAACCTGCTG TGGGGCCATC TGAGTTTGCT ATAGAAGCTT TGTCCAGTCC 350
 GTCAACTGAG CCGGAGATGT GGACCCGGAG CGGGCGGCC CTGCTCGAG 409

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCGGCC AAAGAGGCCT ATAAATATAT AATTGACTTA TTTATTAAAT TTAGGAGAAA 60
 AAAAAAGTTT TCCTTGACAT TCAGCTCTAT TGGATTATT TCCATTTAAT TGCATCATGT 120
 GTTATGTCTT GGTAAACACT CCATTTCCTG TCTTGGTGGG CATCCTGTCT GTGTACCTGT 180
 GCAGTACACT TTAATCATCA AGACTTCAA GTGCTTTTGA GCTATCAAAT CTTGGGAGAG 240
 TCCCATCTAG CATCTTAATA ATTATTTTTC CAAGTTCGTT ATAATTAAC CTTTAACCT 300
 CATCTCATT AATCAATTTT GTATTATCAT TCTGTTGTT TCTGGAAAGC AGCCAATTGT 360
 TCAGCTCTTG AATCAGAATT TTCAAAGACT CACCTCTCT ACCTGGGCTT GCACATATTT 420
 GTCCTAAGTA ATTCTCTATC CCTTAAACCT CTGAGCCCTC GAG 463

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAATTCGGCC AAAGAGGCCT AATTTTGTA AAAGGAATAT CATTCTTTGA TTTTAGATCT 60
 TAGACATCAG GCACTGACAT AGAGCTTAGA TATGTTCTTA AGGTAGCTAA GCCATTATT 120
 ATAGGATAGT CAGATAGGAT AGTTCTAGGA TTTATAGACC TTTTCAGATA CTCTTTATCC 180
 AGTGAGAGAT GACCTATTTT TATTAAACT TGGGTTTGGT ATCTTGGAAT TGGCTTGAAA 240
 ATGATTGTG TTTACATTGG ATGTGAACGG AAAGTTTGTA TCTCAAATGT TTTACCACCT 300
 GAAGGGACAG CTCGAG 316

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGGACATGG AAGTAGGTGA GGTGGGGGA CCTATGAAGA AAAAAAGAGC CTTCCACTG 60
 GGCAGTGAAG TGTGTACACA CACTGCGG GCAGAGCAGT GTGAAAACAT TCTGCACCAG 120
 CACACAAATG ACTTTTGCCA AATCATCTNC CTGATCTGTC GGATGTTACG TCTCTGCAGA 180

```

ATCTGGAGAA AACCAGAAAA CCCAGCTTGT TTGCCCTCAT TTTGGCAGTT TAATTTAGGA      240
ATCACACTGG CTTTACATAA ACTCTTTACC AAAAAAAGTG TATTCTGTAT TTTGAAGGCA      300
CAAGTTAACA TGGGCCCAAG GGAAGGAAGC ATTGTATACA ATTACATAAT AGCTACTCTA      360
TTACTTTAAA ACCTAATGGC AGCCTCGGGC AGAAAAGTCA AAAGGGGAGA GAAACCATTG      420
CTGTGAAATT ATCTGATGCA ATCATCTCTT TGGAGACATT GTCAGTTGAC AATGGTTCTG      480
CTTTTTCTCT CGAG                                     494

```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

GAATTCGGCC AAAGAGGCCT ACGGGAGCAG TTCATGCAGC ACCTCTACCC ACAGAGAAAA      60
CCTCTTGTGT TGAAGGGGAT TGATTGGGG CCATGTACAA GCAAATGGAC AGTGGATTAC      120
CTAAGCCAAG TTGGAGGGAA GAAAGAAGTA AAGATTATG TTGCTGCAGT TGCACAGATG      180
GACTTCATTA AACTTTACCT TTTGACCAGT TGGTCCAGAG GGCAGCTGAA GAGAAACATA      240
AAGAATTCTT TGTTCAGAG GATGAGAAAT ACTACTTACG GTCACTTGGA GAAGACCCTA      300
GAAAGGATGT TGCAGATATC AGAAAGCAGT TTCCTTTGTT GAAAGGAGAT ATTAAGTTTC      360
CAGAATTCTT CAAAGAGGAA CAGTTCCTTT CCAGTGTGTT TCGAATTAGT TCACCAGGAT      420
TACAACATG GACTCATTAT GATGTAATGG ATAATTGTTT AATACAAGTG ACAGGAAAAA      480
AGCGTGTGTG ACTCTTCAGT CCTCGAG                                     507

```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

GAATTCGGCC AAAGAGGCCT AGCTTATCCA GTCTAGTAAT TTTTTTTGTA TGTGTGCACA      60
GCACAAATAG TTACAATAGT TCCCTTTTTT GACATCAAAT TCAACAATAC CTGGCATATA      120
ATTGCTAAAT ACTGTCATCA TTTTCATTAT CATTATCCCC CACATAGTCA TAAATAAGCA      180
CACATGCTAA TCITCAACTC TTCTTCTATT ATTTGCTGCC TTCTTACCTG CGTTAGTGAG      240
AAAGTGCCTT CAAATAGATT GCCAACAGTT ATATGGCTCG AG                                     282

```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

GAATTCGGCC AAAGAGGCCT AGTGCAGTAT TCACGTGTAA C'TTTAAGTT TTCAGTACAG      60
TGCTTTTATA CCTTAAATGC AATGTTGTAT TCATTTGGGT ACTATTGTGT AGTATTTAGG      120
ATGTATGCAT GTTTGTATTAT ATGTAAGCTT GGTGGGTGCT TTCGCTTTTG TGCTACCTTT      180
CTTGATTTT TGTACCAGAG ATGTGCTAAA CTGATGAAAT ACATTGAGAA AGTTTCCATC      240
TTATCTTTT ATATGGGACT GATGATGTGT GTTGGGGTAG ACTGCTCCTG CAGAGTTTGG      300
AAGAAGTCAC CAGCAAAGCC GGCCAATCTC GAG                                     333

```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

GAATTCGGCC AAAGAGGCCT AGGTTTCTAG ACTGGAAGAA CAAATGAATG GCTTAAAAAC      60
ATCAAATGAA CATCTTCAAA AGCATGTGGA GGATCTGTTG ACCAAATTAA AAGAGGCCAA      120
GGAACAACAG GCCAGTATGG AAGAGAAATT CCACAATGAA TTAAATGCCC ACATAAAACT      180
TTCTAATTTG TACAAGAGTG CCGCTGATGA CTCAGAAGCA AAGAGCAATG AACTAACCCG      240
GGCAGTAGAG GAACTACACA AACTTTTGAA GGAAGACAAG GAACGCNAGA AAAAAGACGA      300
AGAAAAGGTG AAGGCAGAGG AAGAATCAAA GAAAAAAGAA GAGGAAGAAA AAAAGAAACA      360
TCAAGAGGAA GAGAGAAAGA AGCAACTCGA G                                     391

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

GAATTCGGCC AAAGAGGCCT AGCTTCTCTG CTTTATTTAT TCATTATTTT TTAATTTTTT      60
GAGATGAAGT CTCGCTCTGT CATCCAGGCT GGAGTGTGGT AGCGCCATCT CAGCTCACTG      120
CAACTTCCAC CTCCCAGGTT CAAGTGCATT GTCTTTTAA TGTCTATGTG AAGGATTCTG      180
AGCTGTACGA GTTCTGCCCC AAATCTGCAC TTGGGCCTCA GGATCAGGCC GCCTCCCCAT      240
CAATCTGGTG GATGCCAGTT ATAACCTTTG CCCTGCACCC CATCCACACT GTAGTTCAGA      300
GAAAATCAAC AGTCAGCAAT CATATCACA GCACTCGAG                                     339

```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

GAATTCGGCC AAAGAGGCCT ACGAGTCAGC ATCTAGACTC AGCTCCTTCT TCCCGCCTGC      60

```

CCTCACACAT GCGTGCAATC ACTCTCCTGT CCAGGCTCAT GTCCTTGTGC CCGCTTGCTG 120
 CTTTGCCCTCC TTGCTTGTTT CTGACTTGCT CACCCACTCT CTGTCAATTGT CTTGCTTACT 180
 CAGGCTCACC CTATCAACTC GAG 203

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCGGCC AAAGAGGCCT AGTTGAATTA TTGCCACATG TTAGGAATGT GGAAGGTGTC 60
 TTGGATAAAT GAGAAAAGAA AGAAAAGAAT GCAAGTAATG TCCTGCTGGG GTAGTGCAGT 120
 CCTCGAG 127

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAATTCGGCC AAAGAGGCCT AGATCCCACG AATTAGGCT CAGAAGCATC GTCCTCTCC 60
 AGCCCTGCAG CTATTCACCA ATATCAGTCC TCGCGGCTCT CCAGGGCTCC CTGCCCTGAC 120
 CTCTTCCCTG GTTTTTCTGC CCCAGCCTCC TCCTTCCCCC CCCCCTATA TCCCTCGAG 179

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAATTCGGCC AAAGAGGCCT ACTGGAATCA CTAACTTTG TCTCATTTTT TTTCTCTTCC 60
 ATCAAATATC AATTTTGGAT TCAGATCCAG TTTTTTCTT TCAATTATTT CTGCCTTTTA 120
 AAATAATACT ACCTCCTTCC TCCCACAATT CATTTAGCT TGTTTTAGTT CCTTGGGTTT 180
 TATATTTTTT CTCCTAGTA TTACAATATA TGCACAAATA TTAGGTATA AACTTCCAA 240
 TACAACTTTT ACTGCCACTC ACAGGTTTTT CAATTGTTTT CATTTTCATG TACATTTAAA 300
 TAATGTATAT ATTAGGATA CTCGAG 326

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAATTCGGCC AAAGAGGCCT AAATATGAAA AGCTGTCTAT ATCTACCCAG CCAAACCATC	60
TCCAGCTTTT ACTTTTATTG AGCAAGTATA CGTTATTTAT TTAGTCATCC ATTCATTCAT	120
TTACTCATTT ATTTATTTTT TTTTCAGCTT ATTTCTGCTT TCATCTTAAT TCCTCTCTTA	180
AACTTTTGG TATCACATTG GTTCTCCCTG ACCTCCACCA CTGTAACCTG ACTTAAGTTA	240
AATGTTTAAT TTATTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	300
TTTAGGTAGA GAAGATGTCT CACCATGCTG CCCACTCGAG	340

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAATTCGGCC AAAGAGGCCT ACTTCTTCC TTATTCTACT TCTCTTTTTT TCTTTTGTC	60
AACATCATGT TTGTGAAAGT TTCAATGCATA TCGTTGCAAG TATTGTATT TCATTCATT	120
CTATTGTTGT ATAATGTTAC ATTGCATGAA TATGCAGCAA TTTGTTCTAC TGTAAAAAGC	180
AATAAGGATT TAGTTATTTT CAGGTTGGAC ACAAATAATT TTGCTATGAA GGGTCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAATTCGGCC AAAGAGGCCT ATAATATAT AGCCTAGAAT TTTTCCTATT CTGTTATTAA	60
GCCTCTATCA CTATTCTTTG ATTCTAGGTT TTATAATCCA TTCTTTTTTA TAACAACCTG	120
TTCTTGTTTT ACTTTTCCCT ATTTTGTGTT TATACCCATC TATTCTTTTT TAGGATCTAT	180
TCTCCACTTT TAACTTTGAG GATTCTAAAA TACTTACTTT AAAGTTATTT TTAACCTGTT	240
CTATTTTGTG TTTTGTGAGG AGCGAATTG CCTTTTTTAT TTGGCTGTTC TACCATGCTT	300
TTTGAATTT TGTTTTGTAG GCTTCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAATTCGGCC	TTCATGGCCT	ACTCTACTCC	AAGTAGGAAA	AGGCCAGGAG	GTCTGTAA	60
AGGATGCACT	CAGAGCCCGG	GCTCCCTAAC	GTATGAGAGT	GCTAACCAGC	AGGTGTAGAC	120
TTTTCAGGAG	TGAAGAATGA	GGCAGGCATT	CCAAACCTGG	ACCTTCATCA	CCTTTTGT	180
CATCTCAAGA	CAATTCTGAG	GGACTGTTT	GGAGCGTGTC	TGGAAGGTGA	ACGTTGAAGA	240
AGAGTGTGGG	CTTTGATGTG	ACTCAGTTGA	ATACTCGAG			279

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCTCAT	GAAACTCTCA	GCGGAAAGCT	ACAAGGAAAC	ACAGATGGTG	AAGATTAAAG	60
AGGAACCCAT	GGAGGTTGAC	ATCCAGGACT	CCCATGTCTC	GATATCACCC	AGCCGGAATG	120
TTGGCTACAG	CACTTTAATC	GGGCGAGAGA	AAACCGAACC	CTTACAGAAG	ATGCCAGAGG	180
GCAGAGTACC	CCCAGAGAGA	AACCTCTTCA	GTCCAGGATAT	CTCTGTGAAA	ATGGCTTCCG	240
AGCTCCTCTT	TCAACTGTCA	GAAAAAGTGA	GCAAAGAGCA	CAATCATACA	AAAGAAAACA	300
CCATCCGGAC	CAATCTCGAG					320

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTCGGCC	TTCATGGCCT	AGAGCAACAT	AGTGAGACCT	CATCTCTACA	AAAAATAAAG	60
AGAAAATTAG	TTGGGGGTGG	TGGCGTGAC	CTATAGTCCC	AGCTACTCAG	GAGGTTGAGG	120
TGGGAGGATC	ACTTGAGCCC	AGGAGTTTGA	GGCTGCAGTG	AGCTGTGGTC	ATGCCACTGC	180
ACTCTAGCCT	GAGTGACAGA	GCAAGATCCT	GTCTCAAAAA	ATAAAGTAAA	ATAAATAAT	240
CAGTCAACAA	CAGTGATTG	TCTTCAAGCT	GCCCTCCTCT	TCGGCTCTCA	AGGCAGTTTG	300
TGAAGTGTCT	AGGATAGGAA	TTTCCAGAA	GGGCTTGCTC	GAG		343

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

GGAAGATGTG CCAAAGTTCA GAAAACATAA TCTTATCTGA TCAGATTAAA GATCACAACT      60
CCAGTGAAGC CAGATTTTCT TCAAAGAATA TTAAGGATTG GCGATTAGCA TCAGATAATG      120
TAAGCATTGA TCAGTTTTTG AGAAAAAGAC ATGAACCTGA ATCTGTTAGT TCTGATGTGA      180
GCGAGCAAGG CAGTATTCAT TTGGAACCTC TGACTCCATC CGAGGTACTT GAGTATGAAG      240
CCACAGAGAT TCTTCAGAAA GGTAGTGGTG ATCCTTCAGC CAAGACTGAT GAAGTAGTGT      300
CTGATCAAAC AGATGACATT CCTGGAGGAA ATAACCCNA CACTCTCGAG      350

```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

GAATTCGGCC TTCATGGCCT ACTCGCGGTC TGTTAGTAGT ATAGTGATGC CAGCAGCTAG      60
GACTGGGAGA GATAGGAGAA GTAGGACTGC TGTGATTAGG ACGGATCAGA CGAAGAGGGG      120
CGTTTGGTAT TGGGTATATG CAGGGGGTTT TATATTGATA ATTGTTGTGA TGA AATTGAT      180
GGCCCCAAG ATAGAGGAGA CACCTGCTAG GTGTAAGGAG AAGATGGTTA GGTCTACGGA      240
GGCTCCAGGG TGGGATGAGC GGGCCAAGAT CGATGATCCC ACAGACTCCA AGCCTGAGGA      300
CTGGGACAAG CCCGAGCATA TCCCTGACCC TGATGCTAAG AAGCCCGAGG ACTGGGATGA      360
AGAGATGGAC GGAGAGTGGG AACCCCAAGT GATTGAGAAC CCTGAGTACA AGGGTGAGTG      420
GAAGCCCCGG CAGCGTCTCG AG                                     442

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

GAATTCGGCC TTCATGGCCT ACAGAAAGTA AGTTGGAACC ATGTAAGAAA AAAAGACACA      60
AATAAACTA GGAAAGTGGC ATGGAGCTAG GCGTGAAGTT GCTGCTCAGT TTACATGTAT      120
GAAGTTCIGT GTGGACTTAA GCTCCTACTT CAGTCATTTA TTGTATGACT TGGACAAGTT      180
GCCAAACATC TCTAATATTC ATTCATATTT GTAGGGTAAA AGGATGAGTA ATATGTATCT      240
TTAGTGATA AAACATTTAC AGACAACTCG AG                                     272

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

GAATTCGGCC TTCATGGCCT AAGACACCAG CGAGCCCAGG CAGGTAATGG AAGCAACTGT      60
AGCTGACTGG ACCTAAGAAG CAGTGGCAGC GGTGCCAGGC ACCCCAGCTG ACCTGCCTTG      120
GTGCTCAGAG CAGCAGGGCT GGCCATGGTC AGGGAGTCTG GGGAGGTCAT GCTCTGTCCA      180
CAGGGTTCTA GCCAGCTTCT GCCAAATTCT CTGTTTTTTC TCAAGAGAAG CTGGGAAGGC      240
CAGTTGTGGT GTCTCATACC TGCAATCATA GCACTATGGG AGGACTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

GAATTCGGCC TTCATGGCCT ATGAAAATTT GGAAGAAGAA TCCAATGAAA GTGCTAGCCC      60
TTTGTACCCT GTTTTGAAG TTGAACCTAA TCTCTAACGA TAACCCAGAG GAACATGTAC      120
TGAAGGTAAT TCCTGAGGAT GCTTCAGAAT CTGAGGAGAA GCTAGACCAA AAAGAGGATG      180
GTTCAAAATA CGAACTATT CATTGACTG AGGAACCAAC CAAACTAATG CACAATGCAT      240
CTGATAGTGA GGTGACCAA GACGATGTTG TTGAGTGAA AGACGGTGCT TCTCCATCTG      300
AGAGTGGGCC TGGATCCCAA CTCGAG      326

```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

GAATTCGGCC TTCATGGCCT ATGGCAATGG TGGTCGTGGT GCTGGGTGGG ATGNGGTCTT      60
CATCCTCTTC CTCCAGGAAG GATGCCTCTG GGATATGGCT GAAGGCCCTCT GGGTGCAGCC      120
TGGCCAGTTT CCCTTTCAGC GTCCTGATAC GCGGGAAGAT GATGTCCAGG TCCCGTTTCA      180
TCTCTACTAG GGTCTCGTG TGGTGCAGGA AGCGTTCGCT CATCTGCTGC AGGCGGGCAT      240
TGGACAGGTT GTTGAAGTTG AGCAGCATCT CATTGGTCTT CTCAAAGCGG TCCAGCATGT      300
TCTTCTGGGA CAGGATGATG GCGTTGACAT CATCTGTGTT CACCATGCTC AGGATGCGGC      360
CGCAGAAGAC CCTCGAG      377

```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

GAATTCGGCC TTCATGGCCT ACATGACACC ACCTGAACGT CTCTTCCTCC CAAGGGTGTG      60
TGGCACCACC CTACACCTCC TCCTTCTGGG GCTGCTGCTG GTTCTGCTGC CTGGGGCCCA      120

```

```

GGGGCTCCCT GGTGTTGGCC TCACACCTTC AGCTGCCAG ACTGCCCGTC AGCACCCCAA 180
GATGCATCTT GCCCACAGCA ACCTCAAACC TGCTCTCAC CTCATTGGAG ACCCCAGCAA 240
GCAGAACTCA CTGCTCTGGA GAGCAAACAC GGACCGTGCC TTCCTCCAGG ATGGTTTCTC 300
CTTGAGCAAC AATTCTCTCC TGGTCCCCAC CAGTGGCATC TACTTCGTCT ACTCCCAGGT 360
GGTCTTCTCT GGGAAAGCCT ACTCTCCCAA GGCCACCTCC TCCCCACTCT ACCTGGCCCA 420
TGAGGTCCAG CTCTTCTCCT CCCAGTACCC CTTCCATGTG CCTCTCCTCA GCTCCCAGAA 480
GATGGTGTAT CCAGGGCTGC AGGAACCTCG GGTGCACTCG ATGTACCAAG GGGCTGCGTT 540
CCAGCTCACC CAGGGAGACC AGTATCCAC CCACACAGAT GGCATCCCCC ACGCACTCGA 600
G 601

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

GAATTCGGCC TTCATGGCCT ATTTTTTTTT TTTTATCAA AAGTTTGTG TATTTTCAAT 60
ACAAATAAA TACCATGCTT GTTACTAGTG CAGTTCTCGA G 101

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

GAATTCGGCC TTCATGGCCT ACAGAATTGG AGGCATGATG AAGACTCTGC TGCTGTTTGT 60
GGGGCTGCTG CTGACCTGGG AGAGTGGGCA GGTCTGGGG GACCAGACGG TCTCAGACAA 120
TGAGCTCCAG GAAATGTCCA ATCAGGGAAG TAAGTACGTC AATAAGGAAA TTCAAAATGC 180
TGTCAACGGG GTGAAACAGA TAAAGACTCT CATAGAAAAA ACAAACGAAG AGCGCAAGAC 240
ACTGCTCAGC AACCTAGAAG AAGCCAAGAA GAAGAAAGAG GATGCCCTAA ATGAGACCAG 300
GGAATCAGAG ACAAAGCTGA AGGAGCTCCC AGGAGTGTGC AATGAGACCA TGATGGCCCT 360
CTGGGAAGAG TGTAAGCCCT GCCTGAAACA GACCTGCATG AAGTTCTACG CACGCGTCTG 420
CAGAAGTGGC TCAGGCCTGG TTGGCGGCA GCTTGAGGAG TTCCTGAACC AGAGCTCGCC 480
CTTCTACTTC TGGATGAATG GTGACACTCG AG 512

```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```

GAATTCGGCC TTCATGGCCT AAATTATTAA AGGTGACAGT ACACAGGAAA CATTACAATT      60
GAACAATGCC TCAGCTATAC ATTTACATCA GATTATTGGG TGCCTATTTG TTCATCATT      120
CTCGTGTTCA AGGACAGAAT CTGGATAGTA TGCTTCATGG CACTGGGATG AAATCAGACT      180
CCGACCAGAA AAAGTCAGAA AATGGAGTAA CCTTAGCACC AGAGGATACC TTGCCTTTTT      240
TAAAGTGCTA TTGCTCAGGG CACTGTCCAG ATGATGCTAT TAATAACACA TGCATAACTA      300
ATGGACATTG CTTTGCCATC ATAGAAGAAG ATGACCAGGG AGAAACCACA TTAGCTTCAG      360
GGTGTATGAA ATATGAAGGA TCTGATTTTC AGTGCAAAGA TTCTCCAAAA GCCCAGCTAC      420
GCCGGACAAT AGAATGTTGT CGGACCAATT TATGTAACCA GTATTGCAA CCCACACCGC      480
TCGAG

```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

GAATTCGGCC TTCATGGCCT ACACACATTG TGAGCTGTAT ACGTTAACCC AAAGTCTGCA      60
TTCAAAGTGG AATTATAACT GGGCAGTGAA TGAGTTGCTC AGTCCATCTA TTAACCATAC      120
TCTTTTAGGC TTTTATTGCT CTCTAATTGT TGTAATAATT AACATTTTCC CAGGAAGTTG      180
TTTTACAGAA GAAGGGGCCT TAGCGGCTTT CAACTCTTTA GAGATAAGTT CAACTTTGTG      240
GATTGACCAC AGCACATCTT GTTTAGTAGT GAGCGGGAGC CATATGAATC CTCTAGAGAC      300
ACAGCCGTGT CTGAGATGGA CATTGCCAAC ACAGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

TTCGGNCTTC ATGGCCTACT CTCATAAAAA TATTCAAAGA TCAACCCCAA ACGTGCCTGC      60
ANTTTGGACA ATGTNAGCTA AAGCTATAAA TGAACACGCA GTGGTCATGG ATGATAAAGA      120
TCAATTATTT CACCCAATTC CAGAGTCTGA TGTGAATGCT ACACAGGGAG AAAATCAGCC      180
AGATCTAGAG GATCTGAAGA TCAAATAAAT GCTGGGAATC TCGTTGANGA CCCTCTCCTT      240
CTTTGTGGTC CNTCTTGCCA TTCTGTAGTG CTACACTGTA CAAACTGAGG CATCTGAGTT      300
ATAAAAGTTG TGAGAGTCAG TACTCTGTCA ACCCAGAGCT GGCCACGATG TCTTACTTTC      360
ATCCATCAGA AGGTGTTTCA GATACATCCT TTTCCAAGAG TGCAGAGAGC AGCACATTTT      420
TGGGTACCAC TTCTTCAGAT ATGAGAAGAT CAGGCACAAG AACATCAGAA TCTAAGATAA      480
TGACGGATAT CATTTCATA GGCTCAGATA ATGAGATGCA TGAAACACTC GAG

```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC	AAAGAGGCCT	AGAAAATAGA	AAATCAGGTA	GCTATGTCAT	TTTATAAGCA	60
TCAGTCCTCA	CCAGATTGTG	CAAGTGAAGA	AAGTGAACA	GAAAAGGAAA	TTAAAAGGAA	120
AGCTGAAGTT	AAGAAAACCA	AAGCAGGAAA	CACCAAAGAA	GCAGTGGTTC	ACCTGAGAAA	180
GAGCACAAGA	AACACAAGTA	ATATTCCAGT	GATTTTGGAA	CCTGAAACTG	AAGAAAAGTGA	240
AACAGAAAAG	GAAATTAAAA	GGAAAGCTGA	AGTTAAGAAA	ACCAAAGCAG	GAAACACCAA	300
AGAAGCAGTG	G TTCACCTGA	GAAAGAGCAC	AAGAAACACC	CTCGAG		346

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC	AAAGAGGCCT	AGGCAGGTAT	TCTTTGCTTT	GGGAAATCT	TCTTTCTGTC	60
CTCCCTTCCC	TCACTTTTTC	CAAATTCTGG	GCACAACAGC	AGCTCTCTCT	CTTCTGTGGC	120
AGGTGTGCAT	CCTATTGGCT	GGCTGGTATT	TCTTGTTTT	TTCCCCCTT	ATTCTTTTAA	180
AATGGGGGTG	GGGGTATAAA	AATATGTGTA	TGGGGTACAT	GCAATAATGT	TGTAATGTTT	240
CTTGTGTGTT	AATGGATAAT	TAATGCAAAA	ATAATTGTTT	TAATTATAAC	ATGTTTGAGT	300
AAATGCTAAA	TTAGTATTTT	TTTCTAATAT	AATAATGAAT	TTGAAATCTA	GCATTCCTGT	360
AACAATGTGT	CTATGTTTGT	CTGTCTGTGT	CTGTCTAATA	GTAATTAATA	TCTGTGGTCC	420
GCACCCACTC	GAG					433

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC	AAAGAGGCCT	AAGCAAAGCT	TAGCTTACGG	GGAAAAAAAA	AAAAAAAAAA	60
AAGTAGAGCT	TNCCTTGAAT	CTGGAGAAAT	TAAGCACACA	GGTGTCTGTC	AATATTAGTT	120
AAGAGACTAC	TGCACCCATC	ATACTGTAGC	TTAAGACAGT	TTCTTCTTTT	AGTTTTTTCT	180
AAAATGTCTC	CATGTCTGTG	TTATGCCACA	AATAACACAG	CCTTGGTTAA	CTTTTGGACT	240
AAAAAAATC	AACTTATTGG	CCAAGCATGG	TGGCTTACAC	CTATGATTGT	AGCACTTTGG	300
ATAGGTCTCG	AG					312

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC AAAGAGGCCT AATTTTCCTA ACTGTGTGCT GCCTTTTGGG TTAATTAGAA	60
TTGTAGCATT TCGTTTIGAT TATTTTITG GCTCTTTAGC TGTCTCTCA CATTTTITAA	120
AATGGTAACT CTAGGGATTA TAATATGCAT CTTTAATTA TCAAAGTCTG TTTTACTAC	180
TTCGTGTAAA ATAAACGAAC CTTGCATTTA TAGTTACATT TATTCCTCTC ATCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC AAAGAGGCCT ACTCAAAAGT AGATGAGCAA TTGGTCAGAA TTGTTAGAGG	60
ATATTATTG AGCTAAATGT TTCCTCTCTC TGTTCAGTG GTGTATGTGC AAGTGTGTGT	120
ATATGTTTTT TGTGGGGAC AGTTTCAGGT AGATGGTATG AAGAGGCAGC AGGAGACTCT	180
CGAG	184

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCGGCC TTCATGGCCT AATTTTCTAA AACCTGGAGA CAAACCACAT AAATACAAAA	60
CAAGTCTGCT TCTTCAAAT TCTGCTGGTG AGAACTCAGA TATCAGTGAT CTTATTAGCT	120
TTTTCACAAG CCAGAACATA ATGGTGACGA TGATTAATGA CAGTGACTAT GTATCCGTGG	180
CTCCCCATAG TGCGGCTTTA AATGTGATGC ATTCAGAAAA GGACTATGTT TTGCGAGCTG	240
TTTCAACAG TACTATGGTT TATTCCTTAC CTATATTAGT GAATATCATT AGTAACTACT	300
ATCTTTATCA TTTAAATGTG ACTGAAACCA TCCAGCTCGA G	341

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GAATTATGCT GTGCTGTTTT CCTGGACACT CAGAATCAAA CAGGCCTTCC ACCCCATCCC	60
ATCATGTTGA ATTACAAAGT ATTTGAGCA TCGTTTGGT TGTTCCTTC CACCCATACC	120
TGTGTAGGGC AGCGGTAGCA GTCTTCAACA ATGCATCCTC TTGGACAATG CATTGTAATA	180

TCTCTCTTTC AAATTCTGTT TCACATAGTC ATTTCTCATG TTCTGTTGGA GACCCCCAAA 240
 AAATTCATTC CACACTGTCA TCCCTTGTG CTAACCAGAA TCTCGAG 287

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC TTCATGGCCT AATGTATGGT AGACAATTTT TTTTAAAGAC ACAGAGATAA 60
 ACGTTTTCCT GCTTTGGTTA CCTTTCCTTT CCCCTTTAAA AGGAATTAGC TATAGAACTG 120
 CTTGTAAAG ATGCTTCTTG ATATTTTACT TTTGTTTCCTT TTCCCTAATC ATTCCCTTTT 180
 CACCCCACTC CTCGAG 196

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC TTCATGGCCT AGTGATTGGG TGCAGAGGAA ACAGGAACCA GAGAAGGGTC 60
 ATCTCAGCTG CCTGTCCAC TCCCTATGCT TGGTGTACC TGCGCCATAG TCTCGAG 117

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GAATTCGGCC TTCATGGCCT AGTAAGTGCT CTGAGTATAT TAGGAAAAGG AAATCTTATA 60
 CATAAAAATC AAAGCTGTTG CTAATTTTTC CACTAGTGAG TCAGTCTATT AACATTACTC 120
 ATGGTAGGTT TTGCCATACA GAATTTTAAT TTTTATATAT TATTTTGGC TTTGTTATTA 180
 TGCTTAGAAG TCCATGGGGA CCCAAAGATC AGAAAAGATT CATCTGTACT CGAG 234

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCGGCC TTCATGGCCT ACAGAACGAA CATTGGCTCG GCGGTGGTGA TGCTAATTC	60
CACTGTCATG TTCACAGTGA TGGCCGTCTT TTCCTTCATC GCCCTCAGCA TGGTTCATAA	120
ATTTTACCGG GGAAGTGGGG GGAGTTTCAG CAAAGCTCAG GAGGAGTGGG CCACAGGGGC	180
CTGGAAGAAT CCACATGTGC AGCAGGCAGC CCAGAACGCA GCCATGGGGG CAGCCCAGGG	240
TGCCATGAAT CAGCCAAGAC TCGAG	265

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTTGCCA CACCATGAAG CTCTTGTCGC AGGTAAGTGT GCACCACCAC ACCTGGAATG	60
CCATCCTGCT CCCGTTTCGT TACCTCAGCG CGCAAGTGTG GATTCTGTGT GCAGCCATCG	120
CTGCTGCCGC CTCAGCCGGG CCCCAGAACT GCCCTCCGT CTGCTCGTGC AGTAACCACT	180
TCAGCAAGGT GGTGTGCACG CGCCGGGGCC TCTCCGAGGT CCCGCAGGGT ATCCCTCGA	240
ACACCCGGTT CCTCGAG	257

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC TTCATGGCCT AGGAAAGATT CGTGTTTAC TTAAATAAAC CTGAAAGAAC	60
TGTCGTTTTT CACTGCCTAT AGGACCACTA CAAAGCCGCA AAGAAAAATT AGACTTGTTT	120
CATTTTATAA CAACAACAAC TGCTACTACT GCTACTAGTT AGATACCGTT TGCTCATTTA	180
TAACAATCTC AGTTGGTAGG ATGAAGCTTA AACACTTGGC ATTCATCGTC TTTTTCAGTC	240
CTCTCGAG	248

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

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GAATTCGGCC TTCATGGCCT ACTGTCTTTT CATGCAGATT TCATATTGTC TTTGTCTTTT    60
TCATTGCTTC TTGACCTTCC TGGCAGGTGT CGCTCAGTTT CTTCCTGTTT CCCTTCCTGT    120
CCTCTCCACA CCTGCTATCC CGTCCCACTC CCATCTACCT CCCGGGAAGC CAGCCCTGCA    180
TGCTGAGTTT GTGACCTGCT TCATTCCCAT TTCATTCTA GAGGGTTTAG AGGTGACCTG    240
GAACCGTTCC CTTCCTCTCT CCTACCCCTT CCTCTGCAAC ACCAAGAGGC CTGGAGGGGC    300
AGACAGAAAG CAGCCAGCCA CGGCGGAAG TCTCGAG                                337

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(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

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GAATTCGGCC TTCATGGCCT AACTTATTTT TTTTGTGAT TGCCTGTCTT TCTTTTCTT    60
TCCTTCCCTC CTCCTCTCTT TCCCTTCCTT CCTTCCTTCT GTAGAGATGA GGTTTCACCA    120
TGTGGCCAGG TTGGTCTGA GCTTAAGTGG TCCTCGCACC TCAGCCTGGC AAACCTGTGG    180
GATTACAGGT GTGGGCCATC ACGCCTGGCC TTACAGTAAA TTCTTGATAA ACAACCCAGC    240
AACACACCTC GAG                                                    253

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(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

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GAATTCGGCC TTCATGGCCT AGGACGGGGG ACTCAGGTTT TACACTGGAA CCTGGGGTCA    60
TGTATCATGT ACCAGGTGGG GAGAAGTGTA GCAATCTCA GTGCCAATTG GAGGGGAAGC    120
CAGTCATTCC AGGAGAAGAG CTGAGGGGAA AGAGCTGTTG ACTTTCATAA TGCACTCTTA    180
ATTATCCAGT CACCTCCTG CCACATGGCA GAAGCCAGGT GGCAGTGATG GTGGTGGGGG    240
AAACAAAACA CACAGTCTCT GGCAAGCCCC ACCGGGAAAG GAGGGCTCAG AAGCCGTAGC    300
GGGTCCGGAT ATCCTCGAG                                            319

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(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

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GAATTCGGCC TTCATGGCCT ACAATAAAAG CCCATAGGGA AGAGAGAGAG GATATAGGGA    60
AACAGAATCA GATGTGTAAT ATACTTGGCA CAGCGAAAAA ATGGATTAA AAGACAAAAA    120
TGGAGGTCCA GGTAGATGTA ATTCACACAG ACTGAAAGTG AGTTCGGGCT TGTGTAAAC    180

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ACATGAGATT GGATTTGACC CCTTGGCTCT CAAGTGTCCT CTTAGATCTA GAACTGCTCC 240
 TTGGTGGCCA TTAGATCGAG TCAGTTTGA TCTGCATCAC TTAGTTATTG GGAATTTCTT 300
 GTTTGAAAC AGGAAATTT TTTAGATTA TTTGGCGTAC GGCTCGAG 348

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTCGGCC TTCATGGCCT AGGCACAGTG AAACCCGTGG AAATTCAAAG GTGAGCAGGA 60
 CAGTGGGTCC TGTATCTTGA TCTTTACGGA TCTTTCTCTT CTTGAATCCT CACAGCACCC 120
 ATTTTATAGA CAGGAAGACT GAGGCCCGAA AGTTCTGTCT GACTCTGAGC CTGGCCTCTT 180
 TGCTGCCTCC CGTTGTCCTG TGAGGCTGTG TGGTCACAGC ACCCAGGACT TGAGAGGAGT 240
 GAAGTTCTTC CTCACCCCGC AAAGGCTTCA TGAGCCCTAC TGTGTGCCAG GCCAGCCCTG 300
 CTCAGTCTGG GGCATAAAC ACAGGCGAGA TTCTGAAAGC CTGTGTGAGG GAAGTTCTAG 360
 GCCTGCAGGA GCTGAGAGGA GACCCTGGAG AGGAAGGGAG TCAGGGCCAG CTCCTCGAG 420

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCGGCC TTCATGCCTA AGCTGATGGA GACTGTAAAT GAACCAGAAA CAGGTGAAGT 60
 GAGCAAAGAT GCAGTCATTG TAAAGCAGGA GAAAAATAAT GAATATTGCC TTCAGGATAT 120
 TGATGATAAA TTGTCAGAAT CAGCAGAGGA TGATGGTGAA GATGATACCA ATGATGAAGA 180
 TGATGATGAA GATAGTAACC CTAAAAAGAA TACTCAGGCC CACTAGAGT TAATGGCAGA 240
 ATTTCTGAGA GCAGAAATGG CCCGAGAGTA CCAGCTGGCA AAAAAATTAT GTCAGATGAT 300
 CCTAATCTAT GAACCAGAAA ATCCTGAGGC CAAGGAGTTT TTCACACTTA TTGAAGAAAT 360
 GTTGCTGATG GAGAAAATC AGAATCATGA GCAAGACGGT GAAACAGTG ATGAAGACAG 420
 CAGCGGGCTC GAG 433

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAATTCGGCC TTCATGCTCT ACAAATCAA CTGCAAGCAG CCATCATCAG TTTGGAAGAA 60
 GCTTTGGGAA GCCTTCAAAG AAAAACCTCG GTATCCACCA AGTCAGGCTC AAGCAGCTCT 120

TCAAGACAGT CCCCTGAAG AGTACTCCTA TAAGAAATCA ATAAGAAACC TGTTTAAAAA 180
 CATTCTTTT GTCCTTCTGT TGATCACTTA TGGTATCATG ACTGGTGCCT TTTATTCAGT 240
 CTC AACGTTA TTAAATCAAA TGATATTGAC ACAACTCGAG 280

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAATTCGGCC TTCATGGCCT ACGCGAGCGG CAGGTGTGCA CAGGAGGTTT TCCACTTTGT 60
 NCTCTGAAGT CGCGGTCAGG ATGGTTTTCT CTGTCAGGCA GTGTGGCCAT GTTGGCAGAA 120
 CTGAAGAAGT TTTACTGACG TTCAAGATAT TCCTTGTCAT CATTGTCTT CATGTCGTTT 180
 TGTAACATC CCTGGAAGAA GATACTGATA ATTCCAGTTT GTCACCACCA CCTGCTAAAT 240
 TATCTGTTGT CAGTTTTGCC CCCTCCTCCA ATGGTACTCC AGAGGTTGAA ACAACAAGCC 300
 TCAATGATGT TACTTTAAGC TTACTCCCTT CAAACGAAAC AGAAAAAACT AAAATCACTA 360
 TAGTAAAAAC CTTCAATGCA TCAGGCGTCA ATCTCGAG 398

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC TTCATGGCCT AGGGCGATGG TGGGCAGAGG ATCCTTAGTG CTCAGTCGGG 60
 CTCCACCAGA ACCACGGAAT TGAAGGAGAA GAGACTCTCG GTTCCAGGTA GCAGAAAACG 120
 TGGAGTTTTG GACACAGATC CTCCTGGCCA GAGAAGGATG CTTGAGAATC TGAGATTTAC 180
 ACAGCTGTAT TAGGTTGTCC ACGATGACCG GGCAGTAGGT CTCTCTCTTG GGGATTTCCT 240
 CAGTGGTCTG CCAGAGACGG GCGTGAGAGA TCACATTCAG AACGCACTCG TCTTGGTTCT 300
 CTATGTGGTT CTTGGATCA TCAACAAGGC TAAGCACTTT CTCGGAAGG CTTCTATTA 360
 ACTTGTCTT GGTGAGCCAG AGGGCCTGCT TTACACCCTC GAG 403

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC TTCATGGCCT ATCCATTTT TCGAATGGCT TATTTAGGCC CAGCTCTTGC 60
 GTTTCATTG TCCTTCAGG CCCAGAACTT TCTCAGTCA TCGTCACCAG GCCTAGCTTC 120
 TGCATCTGGT CAGCCTTTTA AGGCCAGCT TTTGCCTCAT AAACCTCAGT CTTGTTTAA 180

GGCGGCCTCC CGGGTCCCAC TCGAG

205

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC AAAGAGGCCT AGTTTTATTA CTTTGTTAA GACATCAGTT ATTTAGTCT 60
 TTGATAATTC ATTATCTAGA TAATGGTTAC TTTGTATTGT CTGTTTCTCG AG 112

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC AAAGAGGCCT ACACAGAGCC CTTCACTACT TTAAATCTT CTAAATTGG 60
 TGGTTCATGT TAATTAAATT ATTATTATTT TTTTGTGAGA CGGAAGCTCGA G 111

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC AAAGAGGCCT AAAGATGTTT TCCATGAGGA TCGTCTGCCT GGTCTAAGT 60
 GTGGTGGGCA CAGCATGGAC TGCAGATAGT GGTGAAGGTG ACTTTCTAGC TGAAGGAGGA 120
 GGCGTGCGTG GCCCAAGGGT TGTGGAAAGA CATCAATCTG CCTGCAAAGA TTCAGACTGG 180
 CCCTTCTGCT CTGATGAAGA CTGGAAGTAC AAATGCCCTT CTGGCTGCAG GATGAAAGGG 240
 TTGATTGATG AAGTCAATCA AGATTTTACA AACAGAATAA ATAAGCTCAA AAATTCATA 300
 TTTGAATATC AGAAGAATCT CGAG 324

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC AAAGAGGCCT AGGTCCAGAA ACATTTAAAA AAAAAAAAAA GGGGGCTTGA 60
GAAAAGGGCT TCCAGTGCCA GGCAGAAATA TGTTTTCTT AATAGGGC 108

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCGGCC AAAGAGGCCT ATGAAACGTT GGATTTGCTT TGTAACCTG AGAATACATT 60
TTGTTGCCAA CAAAAGAGA GAAGAGAAGA GGAAGATATT GAAGAGAAGA AATCGATTAA 120
GAAAAAATT AAAGAACTTA AGTTTTAGA TTCTAAAATT GCCCAGAACC TTTGTAAGTA 180
TCATATTCCA ATACCATTCA AAGACAGTGG AAATATTCTT TTAATGATT TCATTTCTT 240
TAAGACCGAT TATTCATTAT TTGCTATTTT CATTTTGTTA TTATATGCAT GATAAATTCA 300
CAGATACTCT CGAG 314

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCGGCC AAAGAGGCCT AGGGTAAGAC TAGACTGTTT TAAATCATCA ATAAAAAGTG 60
GAGAAAACAA AGGTATTCA GCGATTGAAT TCTAGACCTG CCTCGAGCCC TGCCTTCCT 120
TTACTTTTAC TTTTTTTTTT TTTTCTTTG GAAGAGAGAA GAACAGAGTG TTCGATTNTG 180
CCCTATTTAT GTTINTANTC GGAACAAAC GTTGGTTGTG TGTGTGTGTG TTTTCTTGTG 240
TTGGTTTTT AAAGAAATGG GNAGAAGAAA AAAAAAATTC TCCGCCCTT TCCTCGATCT 300
CGCTCCCCC TTCGTTCTT TCGACGGTC CCCCCTCAAC CTGCCTCGAG 350

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GAATTCGGCC AAAGAGGCCT AGAGAGTCTG GATGACAAGC AAAGCTCAAT CTCRAAACAA 60

TAATTTTAA AGTAATGATT ATCTTAACCA TTCTTAAATC CTTCTGTCTA GTAGGAATCT 120
TATTCATGGG AGTGTCTGGA AAAGGGACAA AGAGCGGCTA TCTCGAG 157

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC AAAGAGGCCT AGTGTTCAC AAAAGAATTG GAAACCATAG TCCTGAACTC 60
TCCCTAAGTA GTATAAGCTT TAAATAGCAC TCAATCCATA TTAAGTCTTC TTAGTGTAGC 120
ATGGTTGCTC TCATGCGTCT TTCTTATGTT TTAAATGGTG TAAATTTTAS TCGTTTGTCA 180
TTCAGAAAGT GCTTTGCAAA TACAAAATAT CTCGAG 216

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TAATCTTTAC TGGTGAAAAG GATGGAAAAA TAAATCAACA AATGCAACCA GTTGTGAGA 60
AAAAAAAAAA AAAAAAAAAANC CGAAAAAAAA AAAAAAACA CCTGAATGCG GAAGAGCTCG 120
GCTCCCGTTT AGCATTTTGT ACTTAAGGAA ATAAAAAACC AACAAAGGAT CTCACATTTT 180
CTTAAAAAGT GAAGATTGCT GTATACTATT TATTCAACTT ATAATTTATG TTAATCCTTG 240
ATCTTTGTCT TTTGTCATGA CAAAGCATTT ATTTAATAAA GTTATGCATT CAGTTCTCGA 300
G 301

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC AAAGAGGCCT AGTCTCTGTT AATCCTACTC TGCTTTAGCC AGAATAGCCT 60
AGTATTTTAT TTCTATTTTA TATATTGAGA TTTCTTCTAA CATTTCCTTT GATAAAAATC 120
TTCTGCTTTT TGAAAAGTGG TATGTATCAT ATTTTATGT TTCTGGTGTG TCTCGAG 177

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
GAATTCGGCC AAAGAGNCGT AGGGAAAGAT TTCAGCTATT AATCAACTGG AGGAAATTCA    60
AAGCCAGCTG GCTTCTCGGG AAATGGATGT CACAAAGGTG TGTGGAGAAA TCGCTATCA    120
GCTGAATAAA ACCAACATGG AGAAGGATGA GGCAGAAAAG GAGCAGAGAG AGTTCAGAGC    180
AAAAACTAAC AGGGATNTTG AAATTAAGA TCAGGAAATA GAGAAATTGA GAATAGAACT    240
GGATGAAAGC AAACAACACT TGAACAGGA GCAGCAGAAG GCANCCCTGG CCAGAGAGGA    300
GATTCTCGAG                                     310
```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
GGTGGCCTTG GGTCAAGATT CGCACCATGG TGGGCACAAA CCCAGGAGAA CACTTTCCTG    60
TAAACGTGTT TTCATGCTGG AGCCAAGGTT TTGACTTGGG TTTGGATTTT TATTATTTA    120
TTTATTATTA TTATTACCAG GTTGCATCTA AAGGATGTTT TGGAGGAGCA CAGAGTTTGT    180
CTGGTGAGGG TAGGCTCTGG GCAGATTTT CTGTGAGTCT CCCCTGCCTG CGGCATCAGG    240
ATCATCCCTG GTGCCCTGTG GTGGCACCAG GTGGCTGCCC ACCCAGAGGC GTGGCCTTCA    300
CAGTGGGGGC CATCTCAGCC TGGGGTAGCG ATCTGCCTCC GACCTGCCTC GAG          353
```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
GGCCTGCATC GCAACAGCCA GGAGGGCCAG GCCACCCAG GCAGGAGGCA GTGGGCTGGC    60
AGCCACCCTG GGCACAGAAG AGCAGACGCA GACAGTGCTG GGCAACGAGG GGCTTTCTTC    120
ATGGGCCCGC CTGCCCTGTC CCTCCCCCA GGTCCCACC TTCTAGGGTT AAAGTGCAGC    180
TGGGAGGGAG GAGGCAGGCA GAATTGGGGA GCTAGAGAGA GCCCAAGTGA ACCCTGACTG    240
TCCACGCAAG TCCCATGTCC TCCTCGTCCT GGAGTTCCTC GAG          283
```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```

GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAGTTCCTT TTGTTATTTC CCTGCATCTT      60
ACAACGTAA GGCCTTGGTC CTGCTAATA ATAAAATAAT AATCAACTTT ATAAAGAGCT      120
TACAATATGC CAGATACTGT ACTAAGTGCT TTATATTTT TTTTGGGTG GGGGGTGGCT      180
GTTGGGCAGT CTCTCGCTCT GTCACCCAGG CTGGAGGGCA GTGGCACAGT CATGGCTCAC      240
TGCGGCCTTG ACCTCCTGGG CTCAGGCCTC CCGCCTCAGC CTCCCAGGTG GCTGGGGCTA      300
CGGGCGTGCA ACATTCTCGA G                                     321

```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

GAATTCGGCC TTCATGGCCT ACGTAATTCT GGAAAAGTGA ATACTTGTA AGAGTCGTCT      60
TGAATGATTT GTAAAAATC CTGTTCTTAT ATTCACGAG TTTCAATCT TTGTCAGAGG      120
AGTATTACCA TTAGATTGAA AAAAAGGAAA ATAAATAATA AACACTTTTA AAAAACTCC      180
CCATTCTCTT ATTCTCACTT TTAGGAAAAG AGACTGACTA ATATCTTCTG CCACAAATAC      240
CGATGTTCTT AAAAATATTT ATGGGACTGC TTTTGGCAAC CAGCCCTATT TTGTTTTCAT      300
ATCCCTTTT GCTCCCATCT TTCCAAATC ATAAACTCGA G                                     341

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

GAATTCGGCC TTCATGGCCT ACTCGCCTCT ACTAAAAATA CAAAAATTAG CCAGGCACGC      60
GCCAGGTGGT GGCACCTGT AATCCAGCT ACTAGGGAGA CTGAGGCGGG AGAATTGCTT      120
GAACCTGAGA GGTAGAGGTT GCACATAGCG CCACTGCGCT CCAGCCTGGG CAACAAGACT      180
GAGACTCTGT CTCAAAAAAA TATATAAATA AATAAATGAA AAAAAATAAT TGTATAACAT      240
CTATACTATA GCCTCGTAAG CATTAGCTAC TTAATATTTT TGGTATATTT AATAATTTTA      300
ATACAGCATT TTTGATTACT AGTGAACATG AATATTTTCC CATATTTGTT AATTATACTT      360
TCCTCTTACA GAAATTCTGT TTGTGTCCTT CACCCTTCAC TCGAG                                     405

```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC TTCAGGGCTC CTTCTTCCTA GGCTAGTATT TATCCCACTA CATCTGACTC	60
ATTCTCTACT ATCGCTGTTG ATTCCTCTT GGGTACTAAA TCTGTTGAAC ATGTTGCCAG	120
GCTTACTGCT GGTATTATGG GATAGCATTT GCCTGATGGC AGCTTCTAAA GGAGACTCCG	180
ATGGCACTAA GCAGTTTCCA AAAGTTTATC TTGCAAGTTC AACCCAATTC GAG	233

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCTAGA CCTGCCTCGA GATGTTTTTT TCGTTATTTG AAATCTTTGC TCTTTTATTT	60
TTGAGCTCCC AGATCCTCTC CCTCTCTTGA GCTTTCCTG TGTGTGATAT CAAGAATATG	120
AAATGTGAAT TCCACGGACT CGAG	144

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GAATTCGGCC TTCATGGCCT AGGCAGGAAG GAGGCTGGAA TAAATAAAAA TAAAAATAGA	60
CAAGTAAGAC AGCATAAATA ATACATTTTT AACATGTCA ACATTGATAA TACAATGAAG	120
ATTTACCATA AAAAGTATCA TATCTAACCA AGATATGCAA AAGATGCATT CAGTAAGCTG	180
TAACGTTGAG AAATGTAAC GTGAAATCAG CTCACCAGT CAAGTCACTA GGTGTGCCAC	240
TTGGACCGTC TTGGTTTCAG CGAGCATAGC GAGTGGCTGT AAGAAATTGT CCATGCCACC	300
AATTCACATG CTAATTGCCC AGGTGGTCTC GAG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC TTCATGGCCT AGGAAGTGA GGAAGCTGG GTCGCTGCTG GAAGGGAGGG	60
AGGCTGACTC TCTACCCCTC ACCTCTGCAA GGAAGTGAAG CCTGTAGGGT TGCGGCTGTC	120
ACTGGCTACA GCGGCATCT TTCTGTAAAA AGCTTTTCAG GCATGAAACC CATTCTGTGA	180
TGGACTGGGC TGTGTTGACG GTGGTGCTG GGCCTTGTGT GCCAGGCCTC TCTGGGTCCC	240

CTCCCTGGCC TTGCTTCC TCTCCTTC TCGAG

275

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC TTCATGGCCT AGAGTCATAG GTCAGACCAC TTTCTAGGAG CTGTTTCAGTG	60
ATAAAATTAA TAACAGTGAC TTTTGAGTCA AAATAGATTT TTAAAGTACT TGATTTTCTC	120
TTTGATTGG AAACATCTTT GTTTAGCTTA ATTGAAATGA TCTAAAATAT TTGAAGGATT	180
TTATACTTA CACAGAGGCA TGTATTGGA TAATTAGCTT TTATTAAACC CAGGCTTCCT	240
CGAG	244

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GCGATTGAAT TCTAGACCTG CCTGAACCCC ACCCTTCACG TCCTACTTGG GCTGCCAAAG	60
TCATCTTCCC AAAACATGAC TTTTCCTCAG TCACCTTCT TATTAGATTT TATCATATTC	120
CACATCCCTT CCCTGGCCCT CAAGGGTGCC TGTAACTAG AACCATCTTA CCTTCCACC	180
CTTGTTTCCA AACCTCCGC TTACTTAGA CATGCCTCC CATTCCCTC CCGACCCACC	240
CCCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC TTCATGGCCT AGAAAAAAC AAGTAGTTTG GCAAGGAGAG CAGAAAAATA	60
AAATTCCACT GTGTAGGCAT TTGGAGATTT AGCAAGAGCA ACCTAGAGTC TGCCCCCAGA	120
GACACTGCAC GTTGTTTCTG ACACAGAGGA TGCCTAATT CTATTTCCTG TGCCACCTGA	180
AAAAATCATA ATTTGAGAAG AGAACTGTT AGGCCATTTC TAGTGAACATA TTTTCCAAA	240
CCCTCACGGA ACCCTGAACA GGGCGTGTCT CGAG	274

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC	TTCATGGCCT	AAGCTTGCTC	ACTCTTCTGT	GTGTTTGAAA	TAATGGTAAA	60
ATACAATAAT	ATTGTCAAGC	ACAGTGGATC	GGAGATTTT	CTTCTCAGGA	CTATTCTGCT	120
TATAGGTCTA	CTTCCTATAG	CTATTTGTCA	TTGTCTCTCT	GGTCCTTCTC	TTTTCTTCTC	180
TCCTGTGCTA	GATGCTCTCT	CTTCCTATCC	CTCCCTCTCT	TCCCACCCCC	ACCTCCCACT	240
TCTCTGTTTA	TATCCTGATT	TTGGTGGAAC	ACATCCTCCA	GGCTCCCTGG	CACTCGAG	298

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCCTAAG	GTGCCCNAGC	TTGCCAATTA	ATTCCCAGTA	GAAATTTTTA	AATGTTAAAG	60
ACAGTAATTA	AAAAAAAAAA	AAAACCACAC	TGTTTGGACA	TTTACCTCG	TGCTTTGTGT	120
GTGACTAGAT	TATGCACTAG	AATTTCATTC	AGTATTCTTC	CAAATAAGTT	ATTTCCCAAG	180
TGTTGCTGCTG	TATCTAACCA	ANTANTCAAT	AAAGTATTCT	TGCTAAGTNG	GCCATGAAG	239

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAATTCGGCC	TTCATGGCCT	AATATCATGA	TCACTGAAAT	TACATCTAGT	GAAACACACA	60
CGTGCTTATC	TGCACGTGTG	TGTAAGTTAG	AAAGAAAAAA	CAAAGGCCCTA	ACAGTGATTG	120
TCTTAGGTTG	ATAGGATAGT	GGGTGGGATT	TGCAGAAATTT	TGTATCTGTC	AGAAATTTTG	180
CAAAGTGCCC	ATTAGTTTGT	TAAAGAAAAA	AACCTAAATG	TATAACTTCT	AAAGAGATAA	240
TTTTTCTTT	CATGTTTTTG	CTACCTATAT	CTAGGAAAT	AACTTAGAAT	TGTAATTATT	300
TTGAAGCTCT	GGAATTATTA	TGTTCAAAAA	TTACAGAACC	AAAAAGTCTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

GAATTCGGCC TTCATGGCCT ACTTGCTGTG GCTGACTCGG TTATTGACTT TACTTCTTTT      60
CTTTTCAGGT TTTTATGGGA CTGTTTCTAG CCCTGATTCA GGTGTGTATG AAATGAAGAT      120
TGGCTCCATC ATCTTCCAGG TGGCTTCTGG AGATATCACG AAAGAAGAGG CAGATGTGAT      180
TGTAATTCAC ACATCAAACCT CATTCAATCT CAAAGCAGGG GTCTCCAAAG CAATTTTAGA      240
ATGTGCTGGA CAAAATGTAG AAAGGGAATG TTCTCAGCAA GCTCAGCAGC GCAAAAATGA      300
TTATATAATC ACCGGAGGTG GATTTTGTAG GTGCAAGAAT ATCATTCATG TAATTGGTGG      360
AAATGATGTC AAGAGTTCAG TTTCTCTGTG TTTGCAGGAG TGTGAAAAAA AAAATTACTC      420
ATCCATTTCG CTCCAGCCA TTGGGACAGG AAATGCCAAA CAACTCGAG      469

```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

GATTTATTCA TTCTTGATTA AATGCACTGA AAAGTAAAGG GTCTGTTTGT GTCATGTTCA      60
TGAAAATGCG GTTAGAGAGG TGCTATTCAA GTGATTCTGA AGGCACCCCA AGGTATATCT      120
GTAATTTAAA GATTACTGCA AATATCTTTA CTTTACTGTG GGTTTTTAGT ACATCTGTTA      180
ATTAGTGTG TCTTTGTGTG TTTTGTAGAC TAGTGTCTCT CCATCCTTCA ACTGAGCTCG      240
AG

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

GAATTCGGCC TTCATGGCCT AGCATTTTTT TTCTTTAAAT TATTGTATCC ACTAGTTCTT      60
GCCAGTATAA AGGAATACAA TTGACTTTTG TGTGTTTCAT ACGCTACAAC CTTTCTAAAT      120
TCACTTATCA GGTCCAGAAC TCTTCTACTA ACAATGCACT TTTATAAAGC CCTAACACCT      180
CTCCTGATCT CTGTCTCACC CTCCACCTA TCTCACTGTG GGATGGGAAG GAAGTCAATG      240
GAAAACACAG GAGCGCATTG TAATAATAGC CCACATGGTA TACTCGAG      288

```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCGGCC TTCATGGCCT AGCTCGATCC AAGAAGAAAA ATTAAAATGA CAGCTTTTCC	60
CATTGATATA ATCATCTTAC TTTGCTCTCT ACAAGAAATA TGCATTAGGA ACCTTCATTA	120
TAGGTCCACA GAAATAGCAG AACACAAAAG CGCCCCCTA CCCCCCGCC CCGGTAACCA	180
GAAATACACA GAGGCAGAG	199

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GAATTCGGCC TCATGGCCTA GAATTAACCA ATTAAGAATT AATAAATTAC TTATAAAATT	60
AAAAATCAGG AATACCAGGC TTAATGCATT CATTTATTCT ATTTAGCAAA CTTTTTTTTT	120
TTTTTTGAAT GCCCACAATG TCCTAGGTTC TGGAAATACA AAATTACTTG GTACCAGTAA	180
CTCGACTGTC ACCTTTCCAG CCATGGACTT GGTTCAGACA AACCCCCAGT CCACGGTTGT	240
CGTCCACTTG CAGTGCCCGC CGACTGTGGA TATATGCTGG GGATCCCAAC ACAACGCAGC	300
TACTCTCGAG	310

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCGGCC TTCATGGCCT AGTAAATATT TTCTTCTACT TTGTGTTTGG CCTTTTGTG	60
TTCTCAGCAT TATTTTTTGA AGACAAAAG ATTGATTTTG AAGAAGTCTA ATTTATCAGG	120
TTTTTTCTAG TAGTTTGTAG CGGATTTNTG CATGCTGCTT TAAAAAAAT CTTTGCTAAC	180
CCTCGAG	187

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCTAGA CCTGCCTCGA GCCTTGCCCA GAATCAGCAA GTAACTGCA CTAATTGTG	60
TTATATTGA CTTCTAACA CTGATTTTC TGATTTTCC CTGTTGACC CTCCAATTTA	120
TAAAAATGTG TATAATTGTT CTGCTGCTTC TGCTTTTGCC TGCTTTGGCT GCTGCATATA	180

CAGGTGAAGA TCTGGAAAGA AATGATGGAT CTACAGAAAA ACCCTACTTC STAACCCCTA 240
ACCTGCATGG AATTCTGATC AAGAAGCAAC TCGAG 275

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GAATTCGGCC TTCATGGCCT AGTTTCACAT TGTCTGTACT GTGTTGTGCA GTACCAGAAG 60
TTGCTGGTAG CTACTTGGTC TTCTGGGACC TGCCATTGCA GACGTGGTGA TTGTAATCTT 120
AATCTTGTG AACAGGATG GATTTATGAC TGGGATGGCC GGAAGCCACA CCAGACACCC 180
AGTCACCTGG TCATGGGAGA GGTACTTTGT TGGCTTTTCA TAGTACTTAA CACTGTGAGC 240
TGCTTCCTGA AGTGGCACTC TTAAGGCCAG GTGCCCCCAC CCTCGAG 287

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GAATTCGGCC TTCATGGCCT AAGACAGACA TTTTGGCAG AGCATAGATG AAAATGGCAA 60
GTTCCCTGGC TTTCCTTCTG CTCAACTTTC ATGTCTCCCT CCTCTGGTC CAGCTGCTCA 120
CTCCTTGCTC AGCTCAGTTT TCTGTGCTTG GACCCCTCTGG GCCCATCCTG GCCATGGTGG 180
GTGAAGACGC TGATCTGCCC TGTCACCTGT TCCCGACCAT GAGTGCAGAG ACCATGGAGC 240
TGAAGTGGGT AAGTTCCAGC CTAAGGCAGG TGGTGAATGT GTATGCAGAT GGAAAGGAAG 300
TGGAAGACCT CGAG 314

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAATTCGCCT TCATGGCCTA CACCAAGTTG AATCCCTATG CAGGAGGAGA CGGCCTTCAG 60
AACCAACCTGT CCCCCAAGAC AAAGGGCACT CCTGTGCACC TGGGCACCAT CGTGGGCATC 120
GTGCTGGCAG TCCTCCTCGT GGC GGCCATC ATCCTGGCTG GAATTTACAT CAATGGCCAC 180
CCCACATCCC TCGAG 195

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

GAATTCGGCC TTCATGGCCT AACTCCTGG TCATTTTGCA TTTTATCCAG CTTTTCCTCA      60
TCAACCATGT TATCCTGACA GACACATTTA TTGGATATTT AGTTGGAAAT ACCTTATGGT      120
TGGTTGCAGT TGGCTATTAT ATCTATGTAA CTTTCCTGGG ATACAGTGCA TTGCCATTTT      180
TGAAAAATAC AGTAATTCTT CTGTATCCAT TTGCACCTCT GATTCTGCTC AACTCGAG      238

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GAATTCGGCC TTCATGGCCT AGGCTAACGT AATTGAGAAA ACCAAATGAA ATATATCTTG      60
ACCAATAATT TAAAACCATA TCAGAGATTC AGTTTGGTTC TGTCTTCTGC TTTACTGATT      120
TTAGGATCAG CCTCATACAA AAGGGTAATG GTGGCAGCAG CTCCAGAACT CATATCATAT      180
CCTCCCATGT TAAAGTCAA TGAGAAAAGT CTGTCTTCGC CCCAGGATCT CGAG      234

```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

GAATTCGGCC TTCATGGCCT ACTCAGTTCC ATTGTTAAGC AAGGAAAAAC AAACAATACA      60
TTGAATTTGA CAACCCACTG AAGTTGCAGA TAATGAGGAC TTACCATTTG ATACCATTAT      120
TCATCTGGAC CTATATGTTT CACACAGTTG ACACCATCCT ATTACAAGAA AAACCTAACA      180
GTTATTATATC AAGCAAAAAG ATAGTGGGTC TGACAAAAGA TGACGGTAAA ATGCTACGTC      240
ACACCCTCGA G                                     251

```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GAATTCGGCC TTCATGGGCT AAACCACTGC GCACCATATT TCTTAAGGAT GTTCTGAAGA      60
CCCATGAATG TCTGGTCAAG TCTGCTGATC TCTTAATGAG GGACAACCTG TTTGAAATAA      120
TAACAAGCTC CAGGACATTC TACGTACAGG CAGACAGTCC AGAAGACATG CACAGCTGGA      180
TTAAGGAGAT TGGCGCAGCT GTCCAGGCC TCAAGTGCCA CTAGGCCATG AAGGCCGAA      239

```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

GAAAACCCCA GATATTCCTT ATTATGGAAG AAGAAGCAGG AAATATGTTT TTGAATAATG      60
TGGGTCAGAG AATTGTGCAT TTATTATTGC TAGGATGCAT ATACACATTG AACTCAGTCA      120
ACTTACTCTC TCTAAATTAT CTCACCGGTG GAGACATTGC CTCAGGAGTC GAGCCCTGTG      180
GTGTGCCTCC TGCTGTCACC ACATTGACC ACCTAACTGA CCCCCTGTG GTCACCTTTG      240
CCACCAATCT CGAG                                     254

```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

GAATTCGGCC TTGCCAGTAT TCATGCTGTT GCTTCAGTCA AGAATGAATT CCTCAGCGCT      60
ACCTCTCTTG ACCTTCACAT CTTACTTAGT GCAAATGCTG TCTCCTCTG AGACTTGCCT      120
GACTTCGGAT ACTCTCCCTG TGACATCTTA TCTAAAATGT CAAGTGAGAC TCGAG          175

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

GAATTCGGCC TTCATGGCCT AAGTGGCTGT GTGGTATTTT CTAAGTATTT TTAATAATTT      60
TCTCTCATG ATACCCTATA AAAATGCAAC TGTTAAAGAA TTTGTCTTTC TTTCTCATTA      120
TATTCTTTCC AGAGTATATA ACTAATTTAT TCAGCATTC AATTCATTCAG AGATATTTGT      180
TGAGCACTAA CTATGTTTCA GCACTGGGCA GGGATATCGG GATACCAAGA AAGCTCGAG      239

```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

GAATTCGGCC TTCATGGCCT AGAAAATAAT TTAGAGAAAG AATAGAAAGT CATGGAAAAT      60
CTCATAGGTA GGAGACAGAA GAGAGAACAT TGTAATAAG TTTAAAAAAG ATAAGAAAAT      120
CAGGATAAAG TAGTATGGAC TCTGAGGTGG GAGAGAATTT TAAGATTAGC AGGAAAGTAG      180
TGTAATTGGT ACTTTTGTAGT TATTACAAA GCACTCACTT CTTACAGAGT CTCGAG      236

```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

GAATTCGGCC TTCATGGCCT ACGAAGATTA TAATGTATTT TTATTCTGTT TTCAGCTTCA      60
TGTTTCCTGT TGCAGGTGGG ATAAGACCCC CTCAAGGCCT GATGCCGATG CAGCAACAAG      120
GATTTCTAT GGTCTCTGTC ATGCAGCCTA ATATGCAAGG CATTATGGGA ATGAATTACA      180
GCTCTCAGAT GTCCCAAGGA CCTATTGCTA TGCAGGCAGG AATACCAATG GGACCAATGC      240
CAGCAGCGGG AATGCCTTAC CTAGGACAAG CACCCTTCCT GGGCATGCCT CCTCCAGGCC      300
CACAGTACAC TCCAGACATG CAGAAGCAGT TTGCCGAAGA GCAGCAGAAA CGATTTGAAC      360
AGCAGCAAAA ACTCTTAGAA GAAGAAAGAA AAAGACGCCA GTATCTCGAG      410

```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```

GAATTCGGCC TTCATGGCCT ACACATTTGC ATTGTCTGCC CATGGACTGG TTGGAGCAGA      60
AACCTCCATA CCTCAGTCTC TTGGTATTG TCTGCCCCAA CTGCTGCTTT TTGTTGGGAT      120
GTTTGTGTGT GCTGGGGTCT CGGCAGCATC GGCTGCTTCC CGGTGCGCAC TGACATGCAC      180
TTGTTCTCCA CGATGGCTTT CTCTACCTTC TGAGATGCTC CATTATCAGT CCTGCCCTTG      240
TTCCGGAGAG TTGAGATGGT ATCACTTCTC ATCCATCCTT AGAAATACCC CTCTCGAG      298

```

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCGGCC	TTCATGGCCT	AGGGGGCTGG	TAGTGAAATA	TTTGGTACTG	AAAGTGTGAA	60
GACCTCTGCT	GGGGACTGAA	CAGAGGGAGT	GTCTTCTGCT	GGTGGTGTGA	AATCTATCTC	120
ATCATCAAAA	TTATCTTCAA	ATTCTTTAAA	GTCTATTTCT	GGGTCCTTAC	AGCAGGATAC	180
ACAGTTTGCA	ATTAACACTA	TTAATATTAT	TAAACTGCAC	ACACACAGGA	TCACAAAAGA	240
TGAGGAAACT	TCTGCAGCAG	GTGGCGCTCG	AG			272

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC	TTCATGGCCT	ACTACTTATC	ATCCCTGCTC	ACACACCCTT	GTCCAAGGCT	60
TTATGCATCG	GATTTATTTT	TCCAAATCAA	GAGGACAGTG	ATAGATGCAT	TTTCCCCAGG	120
CTGTCTCAGA	AAGGTCGCTA	AATGTATACT	GTTGTCAGAA	TTGCTGAGAT	CTCCCCCAGC	180
TTTTGGTTTT	TGCAGCAGTA	AAACTCTTT	CCACTGTGAC	TTATTTTCTC	TCTCAGGCAG	240
CAGACTCGAG						250

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC	TTCATGGCCT	AGATCTTCTC	CCCATTGAGC	AAAACTTTCC	CATTCCGGTT	60
AATGGTTTTG	ACAAGCAGGG	CACCACGGGG	CATAAAATTG	TATCATCCAG	CCTCCTTCCA	120
GCAGCTCTCT	CCAGTTCTTG	TCTGTGATGA	TGCGTACGTT	GCTCTGCCGC	CTGTGGGTCC	180
AGGGAGCACC	CCCAAGCAAC	AGTACCAGGA	CTGCCAGCGG	AACTGCAAGA	CTCCTGGAGG	240
GTGCCATGTC	TGCCACTTGC	CCACCTCACA	GCAAGCGTGG	CGGCCCAACA	CTAGGTTTTT	300
TAAAAACTGT	GACTATCAGT	GTTTTAAAAA	TTGCCCGGTA	ACTCTAGACT	TCAAAAGTGG	360
GATAAGTAAT	GATAAACCA	TAATAAACC	TGCCTCGAG			399

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAATTCGGCC AAAGAGGCCT AAAAATTAAT ATTACCTTAT GACTGCCTTT ATCATGACTC	60
TCTTAGTGGG GATTCTGTCT CTCCACATGC CCTGGGGGAT GTGCAGCCCC CGTGCACTCC	120
CCGCCTTGGC CGGCCCTTC CCCCATGCCC AGGTAGACTC TGAGCTCTTA GCCCAGCAAC	180
TCGAG	185

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC AAAGAGGCCT AGGGAATAA TCTTAAACAC TGAACCTCTT TTCAGCAAAT	60
TGGCTTTCTA GTTCTCAGC TCTCTCTTA CACCTCTAAA TCTCTTTCCT GGCAAGATCA	120
TTTATTGGC TTGGTTTATG GTGATACTCT TCATTGTTAT ACTGGTGGGT GATTCTTTTA	180
ATTCATAGCT GTTTTTTCT ACTTCAGGAA GATGACACTG CTGGCTCTGC TGGCTCTGAT	240
GTTTACCTTG TGGCTAATGC CTGTGTTTGC CTGTGTTTAC ATTTATTCCA CGATTCATTT	300
GTAAACATTT ACTAAGCTCG AG	322

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCC AAAGAGGCCT ACTCATAACA GCGTCAGAGA GAAAGAACTG ACTGAAACGT	60
TTGAGATGAA GAAAGTTCTC CTCCTGATCA CAGCCATCTT GGCAGTGGCT GTTGGTTTCC	120
CAGTCTCTCA AGACCAGGAA CGAGAAAAAA GAAGTATCAG TGACAGCGAT GAATTAGCTT	180
CAGGGTTTTT TGTGTTCCCT TACCCATATC CATTTCGCCC ACTTCCACCA ATTCCATTTT	240
CAAGATTTC ATGGTTTGA CGTAATTTTC CTATTCCAAT ACCTGAATCT GCCCCTACAA	300
CTCCCCACCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCGGCC	AAAGAGGCCT	ATTATGCTGG	TGCTGTCTAC	TAATTTCAAG	AAAAACTACA	50
AGTCTGGCTA	GACTCTGCTA	CCGCCTAGCA	CTGAGGTGTG	GTCTTTTATC	TGTTATTACA	120
TTCTTCGTGA	TAATGAAATT	CTGAAACACA	TGCTCCAGGC	ACCTTTGTAA	ATGTGAAGGT	190
GAATAAAGTA	TTTGTTTGGT	GTCTGAAAAG	AGATCTTTGA	AATGTTAAGT	TGCCACAGAC	240
CCAGACCAAG	GAGCCTGCTG	AGAGTTTAA	AGGCTCTTAT	TGGATGACAG	TAGATTCTTT	300
CCTTGAAATG	TCTATAATGA	ATATTCAAGA	ATGCTCATTG	TGCATGAAAT	TTGCAATTTT	350
AATTATCAGT	GAAAGAAAAG	ATTACACAGT	GCTAAATGAT	TGCCATGGAA	AAGTTATGGC	420
TACCTCTTGG	AGTAGAGAAA	ATCTCAAAGG	CCGCTACTCG	AG		452

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATTCGGCC	AAAGAGGCCT	AGTGGGCAAC	TTGGAGAAGA	GTGAAAAACA	CTAAAGAATC	60
ATCTCTTTTC	CGAGTCACAA	AGTCCCATGA	ACTTTGTGAC	TCAGAGACAC	TTTTCGTGAA	120
AATTACCTTT	CGGCGGGACA	CCGTCTCAGG	GCAGCTTTT	CAAGGCTTCG	CTTGACATGA	180
TTTCCTTCCC	TTCATCAGTC	ACTTTGGATC	CAGCTGAATA	TCTCTCTCGG	GTGAGAGCGG	240
ATGTGGACTG	GCCTCCACA	GAAGAAGAGT	AGGTGGCTTT	GGTGGGGGTT	GGGGTGCGGG	300
CTGGCTTCCT	GGTCTCGAG					319

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GAATTCGGCC	AAAGAGGCCT	AGTGAAAAGA	AAGAGACTGT	NAAATAATTC	TGCATATCCT	60
CAGTGGATAA	TTCTGTNACC	TATCTGTCAG	CTATTCCATA	TCAATAAAGG	ACACAGCTGG	120
TAATCCAAAA	GGAAAGGATC	TCTTGATGAA	AGTGTCTGCG	CATTCTTATT	AAAGTCAACA	180
TACAAGATAC	ACTCTTAGTG	ATTTTGAAC	CCATAATTAT	ATTTGTCTGA	TAATAATTGG	240
CACTTAACGG	TTACAGAACA	CTTTCAGTGA	TATTTTCCTT	AGTGAATCTT	AACAACAATT	300
CTACCAGTAA	TTTCTAATAT	TTGCCATGAT	TAGACTTTCA	AAATTAGTCC	ACGCACTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTCGGCC	AAAGAGGCCT	AAGAAACATG	GCGGCCGCSA	CGTTGACTTC	GAAATTGTAC	60
TCCCTGCTGT	TCCGCAGGAC	CTCCACCTTC	GCCCTCACCA	TCATCGTGSG	CGTCATGTTC	120
TTGAGCGCG	CCTTCGATCA	AGGCGCGGAC	GCTATCTACG	ACCACATCAA	CGAGGGGAAG	180
CTGTGGAAAC	ACATCAAGCA	CAAGTATGAG	AACAAGTAGT	TCCTTGGAGG	CCCCCATCCA	240
GGCCAGAAGG	ACCAGGTCCA	CCCAGCAGCT	GTTTGCCCG	AGCTGGAGCC	TCAGCTTGAA	300
GATGATGCTC	AAGGTACTCT	TCATGGACCA	CCATTGCTG	TGGCAAGAA	ACGGCTTTAC	360
TTACAAAACA	GTCTCGAG					378

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCGGCC	AAAGAGGCCT	ACTCTGAATT	AATGCAAATT	CCCGTTGTAC	TGTATTTAAT	60
TATGCACAAA	ATGGTGCCCT	TGACTCAGAT	TCAGTGAAG	AAC TTCATT	TTTACTTTT	120
AAGTCTCCAA	GTAGGAAATT	CAATTAGCGT	TATGAAAGAA	ACACTAAAC	TCGAG	175

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GAATTCGGCC	AAAGAGGCCT	AGGCAGCAAT	GTTATCTGTC	CTTCATTCTT	GCATGTTTTT	60
GGAAATGCT	TTTGCTTTTA	CTTTGGTTCG	TCATGGCAAT	CACGTGCCTT	CTCTGGTTCA	120
TTTTGCACAG	ACCTGCCTAG	AGCTGGAACG	TTACCTCCAG	AGCGAGCCCT	GCTATGTTTC	180
AGCCTCAGAA	ATCAAATTTG	ACAGCCAGGA	AGATCTGTGG	ACCAAAATCA	TTCTGGCTCG	240
GGAGAAAAAG	GAGGAATCCG	AAC TGAAGAT	ATCTTCCAGT	CCTCCAGAGG	ACACTCTCAT	300
CAGCCCAGAC	TTTTGTTACA	ACTTAGAGAC	CAACAGCCTG	AACTCAGATG	TCAGCAGCGA	360
ATCCTCTGAC	AGCTCCGAGG	AAC TTTCTCC	CACGGCCAAG	TTTACCTCCG	ACCCCATTTG	420
CGAAGTTTGT	GTCAGCTCGG	GAAAAATTGAG	CTCCTCTGTC	ACCTCCACGC	CTCCATCTTC	480
TCCGGAAC TG	AGCAGGGAAC	CTTCTCAACT	GTGGGGTTGC	GTGCCCCGGG	AGCTGCCCTC	540
GCCAGGGAAG	GTGCGCAGCG	GGACTTCGGG	GAAGCCAGGT	GACAAGGGAA	ATGGCGATGC	600
CTCCCCGAC	GGCAGGAGGA	GGGTGCACCG	GTGCCACTTT	AACGGCTGCA	GGAAAGTTTA	660
CACCAAAAGC	TCCCACTTGA	AAGCACACCA	ACGGCTCGAG			700

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

GAATTCGGCC AAAGAGGCCT AGAAAAATAC TTGGGCAGAA AGAAAAATATC ATCAAATAAC      60
ACCTATTTCT TTTCAGCTAT AGAGATGGCT GGATATCAAA AGCACCACGG GAGCTTTGCA      120
ATTTGCTGCC TCTTTTCAGC CCTCAGCTTG ACTCTCAGTT TTCAAGAGGG AGAAAATGAA      180
TGTTTCCCAG CATTCTCTGT CCTTTGCTCC AAAGAAGAGA GCAGGTGTTG GCTTCCAAAC      240
CTTCCGTATT TTCTTATTGC TGTTAGGGGG ATCAACTGCA TGTTCCTGA GGGAAAAGGG      300
TGGCTCACTG ACCTACTTGA AGGCATTCTC TCAGTGGAAG CTGGGCAAGA GAATCCAGGG      360
ATTTCTTTTG CAGGTTTCTG CGCAGTGCCC CTGCCATCAA GCTGCCTAAA ATGTGAATAT      420
TGCTTCCCTG CGTTTCAGAG GTGGCCGCTC GAG                                     453

```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

GAATTCGGCC AAAGAGGCCT ACAAATGTG AATGGAACAA ACCTGCACGT GTACCCITGG      60
ATGTGTGGAT GTTCTTTGTT TTTATTTGTT AAACCTGATG TCTTGTCTGT ATGACACATT      120
TATTGGAAAC GTTTTTTCCC TATTCTGIGT CTGTGATTTT ATTTTCTCGT GTTCTCCAAA      180
GAGCAGATAT TTTAAATTTT TATATAAATC CAGTTTGTC AATTTTTAA AGGGTTTCATG      240
CTTTTGTAT CCTATTTTCTG AAAACTTTGG CTACTTCAAG GTCACAAAGA TTTTGGATTT      300
GTTTAAATCT ACAAGTTTAA TAGCTTTGAC TTTTATATAT AAGTCTGATT CATTTGGAGT      360
TAATTTTGT GTACAGTGTC AATTAAGGGT CTAGGTTCAT TTATTTTCTT ATGAATATCC      420
AATGGTTCCT CGAG                                     434

```

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

GAATTCGGCC AAAGAGGCCT ACAACACAG AACATTTCCA TCGTGCAGA GAGTACTATT      60
AGAGAGCAGT ATTCCAGAGC CTGTGATCTT AATCACTACA CCTAAAGCCT CCCAGTTGAC      120
AAAGTTACCA CCTTTTTTTG GTGTGTGTGC ACGTGCCTGT GTGTGTGTGT AAGTATATAT      180
AATTTAAATC ATTCCATTAA ATTTACCTCT GAAATTCAAA AGACTGAAAC AGATCTTCTT      240
TTTATCAAAT AAGTTGATTG CAGAGATTAT ATTGGTGTTC ACATTTTCAGG CAACCTGCTC      300
ATGAAATTAT CCATTGCTCT CGAG                                     324

```

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC AAAGAGGCCT ACTCTCCGC CTGCAACCAT TGTTTCCTAC CACTGGATTA	60
TTCTGAAGCA AATTTTAGAC ATCATATATA TTTATCTCTG AAAGAGGACT CTTAAAAACA	120
TGCACCTATA CCTCTATTAC ACTGACAAAA TTGGTAACAA TTCCTTTATA TTATCAAATT	180
TCCTTATTGA GTTCCTGATG TTCAAATTC TGATTCTCCA GATGCTCCAA ACTCCAGAA	240
ACACAGATTC CCAGATGGAA TCCTGGGGAA GGCTCGAG	278

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTCGGCC AAAGAGGCCT ATTTTCTAAT AAAAATATT TTATGGTAGG TTTTGTGGAT	60
TATTGAATAC AATCTGGCAT TCTGTTTAAT ATGTATGTTT TCCTGAATGA GGGGTACAT	120
TGTAATTTTA ATTATTAAC TCACAATGTT TTTGGTTTA AAAATAAAAA TTTTAGGAGC	180
AAGCAGTGT CTGCTTCT TTTCTGAAGA TGATTCTCAA TCGAATGACT CAAGTGATTC	240
TGATAGCAGT AGTAGTCAGA GTGACGACAT AGAACAGGAG ACCTTTATGC TTGATGAGCC	300
ATTAGAAAGA ACCACAAATA GCTCCCATGC CAATGGTGCT GCCCAAGCTC CCCGTTCAAT	360
GCAGTGGGCT GTCCGCAACA CCCAGCATCA GCGAGCAGCC AGTACAGCCC CTTCCAGTAC	420
ATCTACACCA GCAGCACTCC ACCTCGAG	448

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGGCC AAAGAGGCCT AACTTTTGTA ATTTGAATTG GGTCCCGCTT AGTTCTTGAA	60
TTGTTATGAA AATCCTATAT CTGTTGTAT ATTTGCAAAC CCTTTGTATT ATAATTGTTG	120
ATATTITCCC TTTTAAAAA ATACCATTGA AATCAGCATG ACAAAAATAA CACTGTGGGC	180
ACTCGAG	187

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

GAATTCGGCC AAAGAGGCCT AGACCAGAAT AAGCCTTTTA AGGTAAACCT CAAAATTATC      60
ATTTTATGGT AATACTGACC ATTTTAGTCC CCTAGGTTTG ACATGGGAGA TAGTGACTAC      120
ACTGGTGTCT GACTTTTTTC CTAGAGATTT CTCCTGAAA AATACAAGGG CTGTTGCTGA      180
GAGCAGACTT GAGGTGATGA TAGTTGGCCT CTGGTCTACA AAGATTTTAT AACTCCTTGG      240
AAAGCTTCTT ATAATCATTC TTAACCTCTT GGTAAGTACA AATTTAGAGT AGTTGAAATC      300
TTTAGGAATG AACTTCTGAG GGCCAAAAAA TGTGACTGAC AACTCGAG      349

```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```

GAATTCGGCC TTCATGGCCT ACATCACCAA TTCGGCTGGG TAAGGGTCCC CATGAAGGCG      60
CAGCCGGGTA TAGAGGTGCA GGGGAGAGCA GCCTGGGGAG TCCCTATCTG GATAGGCTCC      120
AGCCTGGGTC GGGGCGGTCC TGGTGCCCGG TGAAGCGTCA AAAGAGGGAG CCTGAGCGGG      180
GCAACGCAGA AGGGTGGAGA GGAGGGGGTG GCGAGGGCGG GCAGCGAGGC CTGGAGCCGC      240
CAGGAGAGGG GCGGGGGGCG GCCCTTCTCC AGGAATTTCC GGGGATCGTG TTACAGCGTT      300
GGCGGAGCCC GAGCGGAGTG GGAATCGAG      329

```

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

GAATTCGGCC TTCATGGCCT AGAAAGGGGA GGGAACTGTA CAGGCAGGTG TGGGATAGGG      60
ACTTCTCTTC CGGTCAGAGC AAGGGTCGTC CGAAACCAA ACAACCCTCT TCCCTTCATC      120
TCGCCCCGGA TCCAAAGTCT TGGGGCTAGG CTGGGGCGGG AGTGGCAGCG AGATGTAGGA      180
ACACTGCCTT TCGTTACTTC TCCTGCCATG GCTGACCTTT TTGTCTCTTG TTTTCATGGT      240
TTACACGTAT GAATGGCTTG AGACTGAGGA TTTAGGGAAG AAGCGAAGGC ATCATCTAGG      300
GCTGTGCTGT GCCAAGTTGA GCAGTTGTTT AAAGTGTAG AATTTTGTAC TGGTGTAATA      360
ACCTCTATG CTCGAG      376

```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

GAATTCGGCC TTCAAGGCCT ACGTGAAACC CCATCGGCTT CATTGGCTCC TTGATTAAAA      60

```

CCACGCCCCG CTNTCTGCCC TCTTTGATGC TGCTGGGCCA GGTIGCCCCAG CCATATCCCA	120
GCCCCGTCCTG CAGGGAGCCG GAGGCNGCTG CTGCTGCTAT TGTGTGGATG CCSCGCGTGT	180
CTTCTCTTCT TTCCAGAGAT GGCTAACAGG GGCCCCGAGCT ATGGCTTAAG CCGAGAGGTG	240
CAGGAGAAGA TCGAGCAGAA GATCTCGAG	269

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTCGGCC TTCATGGCCT AGATGTGTTG AACCTTATTC TTGTACATTC ATTCAATCAA	60
GGCAAACTTT TATAATTTT CTTTGTTC CAATGACCTT GAAATGTTAT AGCATGGTAA	120
TATTCTATGC AACTATAGTT ATACTTTTGT GTTGACACT GTATTTTTC ACATTGATTT	180
ACTGGTTGAG GCTCGAG	197

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTCGGCC TTCATGGCCT AGCAAGACCT TTAAAGTATA TACTCTGAAA GTGTGGCTAA	60
TATGATCATG ATGCTGTAGG AAAAAAGGT TATATGTCCA AGTGTATGTA CTTGTAAATG	120
TGCCTAAAGA AACCTGGAAG GATACACAGG TCTTCCCTGG GGTACAAGAC GGAGAACTGG	180
GATCATCATC TTAACCTCTAC TCTTCTTTT TACTCTTCTG TCCTCTTAGA GACTTTTGCC	240
TGTATACATG GATTACTGTT ACTTAGCAGG GCGACCGGT TGGCCAAAGC CTTGGTGTGC	300
CCTTGGCACA ATTCTGCCAA GACCCTTACC CTCTCCTCTC CTCANGGCTC CCTTAACCCC	360
TCTCCCCACA TCTGGAAAAC CCTGGATACA TTTTCT	396

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTCGGCC TTCATGGCCT AGGAAGAGGT TGAGAAGACT CCTGGGCTTC AGCCTCTCCC	60
ACCCAGCCCT GCCCCTCACC TGCTGCCCCT CCCCTCCCC ACTCTATACT AGGGACTGGA	120
TCTCAGCCTC TGATCAGTTT CACAAAGTTT GTTCCCTAAG GAAATCAAAT CCCATTGTCA	180
CCTAACTCTG AAGATCTAAA TAGCCCTTGG ATCAGTACGG GAACCCCAAA TCCCACAGGG	240
CCAGATGTGG AGTCTGTGTC TGCCCCCGTC TTCTCTCCAT CCTCAAAGCC CCCACTTCTC	300

TCCAGGCTGC TTCTCGAG

318

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```

GAATTCTAGA TCCTGCCCTC GGAACAATGG GACTCGGCGC GCGAGGTGCT TGGGCCGCGC      60
TGCTCCTGGG GACGCTGCAG GTGCTAGCGC TGCTGGGGGC CGCCCATGAA AGCGCAGCCA      120
TGGCGGCATC TGCAAACATA GAGAATTCTG GGCTTCCACA CAACTCCAGT GCTAACTCAA      180
CAGAGACTCT CCAACATGTG CCTTCTGACC ATACAAATGA AACTTCCAAC AGTACTGTGA      240
AACCACCAAC TTCAGTTGCC TCAGACTCCA GTAATACAAC GGTCAACCACC CTCGAG      296

```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

GAATTCGGCC TTCATGGCCT AGTCTCTTGA AAAGCCGCAT TTCCAGGCGC TTGGCCAGTG      60
GCCTGGGAAG TAGCCTGTGC TTGTATTGAG ACAGTCCCCC AGCAGCAAAC CATGTTCCAG      120
TCATTCCCTT TCCTACTTTG GGGATTGTTG CCTTTTCTGC TTGTTTAAAG TAAAAACAAGC      180
ATGTACTTGT TTGTATGTAT GTATGTATGT AGTTGTACGG TGGGCACAAA TAAAAAGAGG      240
GCTGTATCCA AATAAATCAT TTCTGGCTGC TCACTGGCAC AGTCCCTTTG CTCCTGCCCC      300
TCCTGGCTCG AG                                     312

```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

GAATTCGGCC TTCATGGCCT AGGCAGCGTT TCACCGCTGT GGAGGACCAG TATTACTGCG      60
TGGATTGCTA CAAGAACTT GTGGCCAAGA AGTGTGCTGG ATGCAAGAAC CCCATCACTG      120
GGAAAAGGAC TGTGTCAAGA GTGAGCCACC CAGTCTCTAA AGCTAGGAAG CCCCAGTGT      180
GCCACGGGAA ACGTTGCCT CTCACCTGT TTCCCAGCGC CAACCTCCGG GGCAGGCATC      240
CGGGTGGAGA GAGGACTTGT CCCTGCTGGG TGGTGGTTCT TTATAGAAAA AATCGAAGCT      300
TAGCAGCTCC TCGAG                                     315

```

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

GAATTCGGCC AAAGAGGCCT AGGAAGATGG CGAAGGTCTC AGAGCTTTAC GATGTCACCT    60
GGGAAGAAAT GAGAGATAAA ATGAGAAAAT GGAGAGAAGA AAACCTCAAG AATAGTGAGC    120
AAATTGTGGA AGTTGGAGAA GAATTAATTA ATGAATATGC TTCTAAGCTG GGAGATGATA    180
TTTGGATCAT ATATGAACAG GTGATGATTG CAGCACTAGA CTATGGTCGG GATGACTTGG    240
CATTGTTTGT TCTTCAAGAG CTGAGAAGAC AGTTCCTCTG CAGTCACAGA GTCAAGCGAT    300
TAACAGGCAT GAGATTTGAA GCCATGGAAA GATATGATGA TGCTATACAG CTATATGATA    360
GGATTTTACA AGAAGATCCA ACTAACACTG CTGCAAGAAA GCGTAAGATT GCCATTCGAA    420
AAGCCCAGGG GAAAAATGTG GAGGCCATTG GGGAGCTGAA TGAGTATCTG GAACAATTG    480
TTGGAGACCA AGAAGCCTGG CATGAACCTG CACTCGAG                                518

```

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

GAATTCGGCC AAAGAGGCCT AATTGAATTT CATTTCTTTT GTAGACTAAT GTTACAATAA    60
ATAAATGGGA ATTTTAAATA CCTGCACTGT CTGTTTTTCT CTTTTTCTT TTTTCAGCCA    120
TAATGAAAGG AAAGTGACCT GCAAACATCC AGTCACAGGA CAACCATCAC AGGACAATTG    180
TATTTTTGTA GTGAATGAAC AGACTGTTGC AACCATGACA TCTGAAGAAA AGAAGGAACG    240
GCCAATAAGT ATGATAAATG AAGCTTCTAA CTATAACGTG ACTTCAGATT ATGCAGTGCA    300
TCCAATGAGC CCTGTAGGCA GAACTTCACG AGCTTCAAAA AAAGTTCATA ATTTTGGAAA    360
GAGGTCAAAAT TCAATTAAAA GGAATCCTAA TGCACCGGGC GATCTCGAG                                409

```

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

GAATTCGGCC AAAGAGGCCT AGTACAGTCC CAATCAAGAA GCCTTATTAA CCTTCTGTGT    60
GAGGGACTAG ACTCAGTGTT GGGTTTGGAG GATCCACTGG TGAGGAGCAT TCAGTCTAGC    120
AGGAGAAATG TCAGCATTAT TTATTACACA ACAAGATCTG ATGCATTACG ATGTACTTAC    180
AGGTCTAGGA ACTGTTTCTG GGAGCACAAA TGAATGAGAG AGAGAGGGAG AGAGGGAGAT    240
TGAGTGAGTT AGAGAGTTGT TGGTGCTCCA CAAGGAGCAG TAAAGTATTT TAAAAATAAA    300
AAATAATAAG GCTGACTCTG TGTCTGCTCT AGGGGTTGGC CATGCTCCAC AAAAAGCAGT    360
AAAGTGTTTT TTGTTTTGTT TCGTTTTTTT TTAAAGACA GACGTCTCGA G                                411

```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

GAATTCNGCC AAAGAGGCCT AGTTTATCT TCTTACCTAT TTAAGTGAATG CNACATTACT      60
GCACACCAAG ACAAAGAGC TCTCCAGGAA AACATTGGAT ATATTGAGAG CATTAAAAGA      120
TACTGCAAAA GCTCTAATAA ATTCAGTCTG CTTATTTTCC AAATTCATA AACTACATAC      180
TTAGGAAACT GTGCTTTCAG TGAGCTAAAC TTCTTTTTC AAGTAACTAT CATAGTTTTC      240
AGAAAAACAT TTTAAGAAGA CAAAAGTAT TTATTAAGCC CATCTAAAAG GCTAATGCAA      300
ATTCCCAAAA AAGGAGCACA TAGAGATAGG CATCTCGAG                               339

```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCCT CGAGACACTA GCCCTTTTTC      60
CTGTTGGTTT AGCACAATAA CTTCCCTCCT CCGGCACCTC CAAACCTACC CCACAGTCAG      120
TGTACTTGTT TTATATATAT TTAATCTTAT TCAATGGAAA CCATGCTTTT GTCGTTTTCAT      180
ACTTGTCTAG GTAGACTTCT CGAG                                              204

```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

CTCGAGAGGC GCATCTTCAC TGGCATATGA CAGGCTGTCA CTGCAGCTAA TGTGGGTACA      60
GTTTTTCCAA AGACCTACTG ATGCATCTAC CGTATTGGAA ACCAACCAGA CATTGGCAAT      120
GGTGCTAACA AATAGCATAA TAACAGTAGC GATGTGGACC ACAAAGATAC CAGCCAGCAA      180
TACCAACATG TTGGCTCTTT TTTTCTTGGT AACTTGTGAG CAAAGAGAGT TCTGAAGGGT      240
CCCAGCGACA GAGGCACTCG AGGCAGGTCT AGAATTCAAT TAGGCCTCTT TGGCCGAATT      300
C                                                                           301

```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC AAAGAGGCCT AAAATATTTG AGTCTAACT TATAAATTT GCATTCTCCC	60
TAACGAAAAA ATTTCTATTA CTGTGGTGA TTTCTTTAAA TTTTGAATAT AGTTACTGAA	120
ATATTAATTC TTTCAATTAA ATTTATATTT ACTCACTGGT TCCTTCCCCT TCTTTAAGGA	180
GACAGAAAAC ATTAACACTT TTAACTCTCT CATTTGTTA AAAATTATT GACCTCTCCT	240
CTGAGACAGT TTGTATTCCT AGATCTCTTT AAACATAAAT ATGCTTATTT TCAAGTTTTT	300
GTCACAGTAT TCACTCGAG	319

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC AAGAGGCCT ATTTAGATTT AACCCAGTTT GTAGACATTT GCATAGATCA	60
AGCAAACTA GAAGAGTTTG AAGAGAAAGC ATCAGAACTT TACAAGAAAT TTGAAAAAGA	120
GTTTACCGAC CACCAAGAAA CTCAGGCTGA ATTGCAGAAA AAAGAGGCAA AGATTAATGA	180
GCTTCAAGCA GAGCTACAAG CTTTAAAGTC TCAGTTTGGT GCCTTGCCAG CTGATTGTAA	240
TATTCCTTTG CCTCCCTCTA AAGAAGGTGG AACTCGAG	278

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC AAAGAGGCCT ACCTGGCTCA TTTATAACCT CCTCGATCCT ATTACTGATT	60
TGCATTCTTA ACTACAGGTA AGAGAAAACC AGTGCAACCT AGCTTTCAAT AGACAGGAAT	120
TTGCTGGCTC ATATAAATGA GACATCCAAT AAAGAAGAAA AGTTGGAAAA AATGTGTCAA	180
ATGTAGCATC CTCTCTCTCT CTCTCTCTCT CTCTCTGTTT TTTCACCTAG GCTTGTGCCA	240
TAAACCTGCT TCTACATCAG TTACTGTGGT TATGGGCGTC TTGTTGGCTG AGCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```

GAATTCGGCC AAAGAGGCCT ACTTAGCAGA ATATATTCTT TAATAGCTCC CATAAAGCAA      60
ACAAACCCAA AATATATTCT CCTGACCCTA CATTCACTTC CAACTATCAC CCTACATCTA      120
CATTCTCCTT TTCATACCAA ACTTTTTCCT AGCAGTTGTC TATATTTATG TCTCCACTTC      180
TTTACCTCCT ATTCTTGCTT CAGTATGCTT CAGTTGAGCT TCGTCCCCTT GTAGTCCACC      240
ACCAACTCGA G                                                                251

```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

GAATTCGGCC AAAGAGGCCT AGATTGATTC TGTGTTGTGG TATTGGCCCT TACATACAAC      60
TGGAGGAAGT GTGAATTTCAT TCATGTTGAT AAATTGGACT GTCATGATTC TTTATAATTA      120
CTTCAATGCC ATGTTTGTCTG GTCCGGGCTT TGTCCCTCTG GGGTGGAAAC CGATGTGTGA      180
TGAAGATGGA CCATCACTGT CCTTGGATCA ACAACTGTTG TGGTTACCAA AATCATGCTT      240
CGTTCACACT GTTCTCCTT TTAGCACCAC TGGGTTGTAT CCATGCTGCT TTCATTTTGT      300
TGATGACTAT GTACACACAG CTTTATCATC GGCTCTCCTT TGGGTGGAAC ACAGTGAAGA      360
TCGACATGAG TGCAGCACCC TCGAG                                              385

```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

GAATTCGGCC AAAGAGGCNT ACCCNGATTA TAGTTTTTGT ATTGTTTTTA CAATTTTGT      60
GAATTAGGAT CCAAATAAGG TCTGTAAATA TTACATTGGG TTTAGGTAAT CGATACTTTT      120
TTTCTTTTAA TCTATAAGTT TTCCTCTATC TTTTATTGTG GGTATTCCCT ATACAATTGG      180
TTTGTGTAAG AAGCCAGGTC TTTGCCCTAT AATACTTCTC AGAATCTAGA TTGTGTTGAT      240
GAGATCCCAG TGGTTTCATG TAATATGTTT TTTTGTCCCT TGTATTTTCT GTAAATTTTG      300
TTTATTTTAT TTTTATTATT TCTATTATTT GAGATGGAGT CTTGCACTGT CACCCAGGCT      360
AGAGTACAGT GGCATGATCT CAACTCACCG CAACCTCGAG                               400

```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

GAATTCGGCC AAAGAGGCCT AAGAGCCTAT AAGGTTTACA TATTTCACTG GAGAGAGAAA      60
TAGGGACATA CAATAAATGA TTTTATAATA AATTTCCATG AAAAGTGAAT CTGAAAACCC      120
CACCGGAAGG CAGAGTAGTG CAGCCAAAGG AGCATGAATT GTGGAATCAT ACAGCTCTAG      180
GTTCAGATCC TACCTTTACC ACTTGATAGC TAGGCAGACT TCAACAAGTT AGTCTAATTT      240
GAGCTTCAGT TCTTCATCT GTGAAAAAGA GAAAATACAG CCACCTTTATA ACATTATTTT      300
AGATGCCATA AGGTAGGTAA AGTGCCAGAC ACATAGATTC AAAAATCTCA ATAAATAGG      360
AAGGCTGGAA TTTCCAAAAT TTTTCTTGC TTTCACAATC TGGGTCTCTAA ATTTATTATT      420
ACTCTACCCA TCACTTCCTC CTCTCCCTC CACAACCTCA CTATAAGCCC AACATCTCGA      480
G                                                                                   481

```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

GAATTCGGCC AAAGAGGCCT AGTGTCACTG AGAGGTCTCA GCATTTCTCT TAGTATTGTA      60
CTGTATTAGT TTTACATATT TCTTCTTTTG TTTAGAGTAT AACCGCTTCT TACATTTCCT      120
TCAGTCGTTT TCTAAAGAAG AAATTAATCT TTTAGAAAT CCTGGCAGTT ACCCCGCAAT      180
TGATGTTTTG GTGAAAATT AGAGCACACC AGTTTGTCAT AACTTTAAGA AACATTTTCA      240
CTTTATTGAT ATTCTGAGGA TTTTAGTGAT TTGGGTAATT TGGGTCTAAT AAAGAGTAAA      300
TTGTTGAATA CTCATTGTG TTGAGTCATC TATATTTTAA AACCTTTCT TTAGTTGTTT      360
TTTCATCCCT AATACAAATG CAACTTCCC ACTTGCTCGA G                                                                                   401

```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

GAATTCGGCC AAAGAGGCCT AAAGTATGTT CTTCATTTG CTGGATAGGA CATGCTGACT      60
GATGACCTCA CAGACTGTTT TTATGCCCTC ACTACTCACC TCACCACCTA CAGTCATAGG      120
CTGACTAGGA GTTGGTTGTG TACATTCCCTA AACCTTTTGG CCCTCTTTAT TTGTCTTTCT      180
AAGTGTGTAT TCAGTACTAT GTAAATTGAT AAAACATGAG TGTGAAAATA TTTTCTTTTG      240
CTATAAAAAA GTAAATTGAA TTCTTTGGGG AAGAGCTGAT AAAATATGTC ACTTAAAGAT      300
CTTGTTAAAT TAGATGAGGG AGATATAGAT GACAGAAACT CTTTCAACAA ATATCTAAAA      360
AGATGTGCCA CTCCAATTAT TTTGTGAGTG TCTTCAAGTT TTTGTCCAC TTTAAAGAAA      420
ACCAAATGCG CCATCATAGC CAATGAATTA TGCAGGAGTC TCGAG                                                                                   465

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

GAATTCGGCC AAAGAGGCCT ACACATTATA TTAGATTTC TAGAACTGT TGGAAATATC      60
TAGCACATGT GCTTATCCC ACAATAATTA CATAGAAAAT TAAAAAGAAT TAATTCTAAT      120
GTAACCATCT TTTTACTTGA CTTTTTTTTT TTTTGCTCTG CTCACAGGTC TAATTGTTGT      180
TATTCTCACT TTATTTTCT ATAAGGTAGG AATAATATCC ACTTCATTAG CTCATCATGA      240
GGGATAAGTA GGATTGAAA AGATACTTTC AAAGGGCACC TAACTGTGAA GAAGATGCCT      300
TCATTGTCAT TTCTTCTTG GCACATTCTCT TGTATCCAG TCATTCATTA GGACTCCATG      360
TTTATTGAAC ACCTACTCTG TGCCAGGCAC TTTTCTCTGT TCTGGAAATA TCACCATGTA      420
AAAACAAATA GCTGAAGAAT GCCCTGCCCT CATAGAGCTT ACAGACATAG AGCTCGAG      478

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

GAATTCGGCC AAAGAGGCCT AGCGTTTCTG ACTTTATTAC TGGTAATTTA TTGCACAGGT      60
TTTCTGTCAT CAAAAAAGTA TCTGCTAAAA TAGAGAAAGT TGTGCTGAA TTCACATTTC      120
CCCCCAACTT CTAATAATAT TTCCCTAAA AAAGAATCCA CTCATCTAAT TTTAAAGAAA      180
ATATACTTCT TACACAAGAC AATCCAACT GATGCAAAAT ATTTATTCCA AGTTAGTTAT      240
TTTATGCAGT AGTTTCCCCC TCGAG      265

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

GAATTCGGCC AAAGAGAGAA ATTTTAATCT TGAAAGACTT TTCAGGGTAT CTCATTTTTT      60
AGGTGGGGGT GGCAGGTGTA TTTCTTTTTT AACAAATAAA AGGCATTAA GTAAACTAA      120
AATGAAAAAA GTAGGCCTTC TGACATTGTG TACTTGGTGG TTCTGTCCCT CTGCCTGTAA      180
CAAATCTCAT TTTGTTACC AAGAACTGTA TGAAAGAAGT AAATCCACCC CTCTCGAG      238

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

GAATTCGGCC AAAGAGGCCT ATGCCTGTGT TGGGTTGACA GTGAGGGTAA TAATGACTTG      60
TTGGTTGATT GTAGATATTG GGCTGTTAAT TGGTGTGTA GAATATTGTA GCACAGGTGG      120
AGTAGAAACA AATCACAAAG ACTTTAAGGA GTTGAGGTAT AATGAAAGTC TCACAAACTT      180
CAGCTGTCAT GGAAGAATG GAACCACCAA TGGAAAGGATC ACTCATGGTT TCAAGTTACA      240
GAGTGCCATG GAGAGTGGCC TGATGCCTTA CACGAATTAC ACATTTGATT TCAAGGGTAT      300
AATAGACTAC ATTTTCTATT CTAAACCTCA GCTGAACACC TTAGGCATCC TGGGCCCTCT      360
GGACCACCAC TGGCTGGTTG AGAATAACAT CAGTGGCTGC CCGCACCCCTC TCATCCCCTC      420
TGACCACTTC TCACTTTTTC CACAACCTGA GCTCTTACTG CCTTTCCTGC CCCAAGTCAA      480
CGGCATTCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

GAATTCGGCC AAAGAGGCCT AAGAAATCAA AATTAAAGCA ATCAAATAAT ACTCACATTT      60
ATATAAGAAA TACTTCAATT TACTTTCCAA TGAGTAAAGT TTTATATTGA ATGTTTTAAT      120
ATTTTCATATT TAGTTTCTT GCAATTATTT ACTTTTCTA AAACCTACTT AAATTAGGTT      180
TAAAAGTCTA CTATATATAA TTGAAATTT TATTCAGTTT GCCTACAGGT GTGTTTTAAC      240
CACTGTGTAC ATAGTATTTA ACGGTCTGCT TTTTTTTTT TAATATGGT TCATGNTGA      300
ACATCTGTAT GTTCATACTT TTCTTGACAA AGTCTAAAG GTTACTGTGT TGAAGCATAC      360
TGAACGATTA CTGATAATTT CTATTTTGAG GAACAGGTAT GTCAGTTCTT TCTCTCTGTT      420
TGATAATTCT CTCTTTTCCC CTTAGGAATC CAAAAATCCT TGTGGAGTGT CTTACTCCTG      480
ATTTTCGAGG TGATCTCAA GCAATAGAAA AAGTTGCTCT GTCAGGATTA GATGTGTATG      540
CACATAATGT AGAAACAGTC CCATTGCTCG AG

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

GAATTCGGCC TTCATGGCCT ATCGAGATAC GCTTTCGCGC ACCAGGTACG CCTGGTGTTT      60
CTTTGTGGTT TTTTCGATTG TTTTGGGGA GTGCGGGGAG TCACAGTTAG AAGGCGGCCG      120
GGTGTGCTG GAGGAAAGTG CTGAGGTCCA GAGCGTAGTC CGAGGGCTCC GAAGTCAGAT      180
TAAAGGGCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

GAATTCGGCC TTCATGGCCT ACATAATGAT GCTGCCTCAA AACTCGTGCC ATATTGATTT      60
TGGAAGATGC TGCTGTCATC AGAACCTTTT CTCTGCTGTG GTAAC TTGCA TCCTGCTCCT      120
GAATTCCTGC TTCTCATCA GCAGTTTAA TGGAACAGAT TTGGAGTTGA GGCTGGTCAA      180
TGGAGACGGT CCCTGCTCTG GGACAGTGA GGTGAAATTC CAGGGACAGT GGGGGACTGT      240
GTGTGATGAT GGGTGGAACA CTA CTGCCTC AACTGTCGTG TGCAAACAGC TTGGATGTCC      300
ATTTTCTTT CGCCATGTTT CGTTTGGAC AAGCCGTGAC TAGACATGGA AAAATTGGC      360
TTGATGATGT TTCCTGTTAT GGAAATGAGT CAGCTCTCTG GGAATGTCAA CACCGGGAAT      420
GGGAAGCCA TAACTGTTAT CATGGAGAAG ATGTTGGTGT GAACTGTTAT GGTGAAGCCA      480
ATCTGGGTTT GAGGCTAGTG GATGGAACA ACTCCTGTTT AGGGAGAGTG GAGGTGAAAT      540
TCCAAGAAAG GTGGGGGACT ATATGTGATG ATGGGTGGAA CTTGAATACT SCTGCCGTTA      600
TACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

GAATTCGGCC TTCATCGCCT ACAGCGCTGC CTTTCCTTAT GAAGAAGACA CAAACTTGGA      60
TTCTCACTTG CATTATCTT CAGCTGCTCC TATTTAATCC TTTCGTCAA ACTGAAGGGA      120
TCTGCAGGAA TCGTGTGACT AATAATGTAA AAGACGTCAC TAAATTGGTG GCAATCTTC      180
CAAAAGACTA CATGATAACC CTCAAATATG TCCCGGGAT GGATGTTTG CCAAGTCATT      240
GTTGGATAAG CGAGATGGTA GTACAATTGT CAGACAGCTT GACTGATCTT CTGGACAAGT      300
TTTCAAATAT TTCTGAAGGC TTGAGTAATT ATTCCATCAT AGACAACTT GTGAATATAG      360
TGGATGACCT TGTGGAGTGC GTGAAAGAAA ACTCATCTAA GGATCTAAAA AAATCATTCA      420
AGAGCCGAGA ACCCAGGCTC TTTACTCCTG AAGAATTCTT TAGAATTTT AATAGATCCA      480
TTGATGCCTT CAAGGACTTT GTAGTGCAA ATCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

GAATTCGGCC TTCATGGCCT ACCTTGATAC ATCAGCTGAC CTCATTCCG GATACCTTT      60
CCCCCCGAA AAGTACAACA TCTGGGCCG CCCAGCCCGA AGACAGATCG TCGTCCCTG      120
GACAATCAGA CGAATTCTCC CCCCCCGC AAAAAAAG CCATCCCCC GCTCTGCCCC      180
GTGCGACATT CGGCCCGC GACTCGGCCA GAGCGCGCT GGCAGAGGAG TGTCCGGCAG      240
GAGGGCCAAC GCCCGCTGTT CGGTTTGC GAACGAGCAG GGAGGTGGG GGCAGCGTCG      300
CGGGCTTCCA GACACCAATG GGAATCCAA TGGGGAAGTC GATGCTGGTG CTTCTCACCT      360
TCTTGGCCTT CGCTCGTGC TGCAATTGCT CTTACCGCC CAGTGAGACC CTGTCTCTCC      420
AG

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

GAATTCGGCC TTCATGGCCT AAGAGATTAA GTGATTTACT CAAGGTCATA TTCCTTGGA 60
GTAGCAAAAC TTCTGGACCA GATTTCTGAT TCCAAAGGCG GTACTGCTTG TACAACACTC 120
TGAGAAGTAA TTACTGTGGA GCAAAGCAAA AAGAAAGTCTA AAAGCAGGTG ATAGGTGTAG 180
ATTTAGATAG TGTAAGGGTA GGCTAAAGTG TTGTAACAAA TGCACCCTCA AGTAGGTAAT 240
GGCTCAAACA CAATAGATGT TCACCTCCCA CATCTCAGAG CAAATTGGGT TCTCCTCATC 300
AGCTAAAGCT TTCCTACATG GGATGATTTG GGGAGCAAGA CACTCCATCT ATGGCTCCCT 360
TACCCTCCAA GGCCTTCTTA TTGTCTTTAT GTAACCAGTG GAAGAGCTCG AG 412

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

GAATTCGCCT TCATGGCCTA GGCTTCTTCG GAGCTGTGTA NTCTTAATTT GCTTTGCTGC 60
TGGCTGGCTG ACAGCTGATG GGGGACTCCT CANGACGGAC TCCCTTCCAG ATGCACCCAT 120
CTCCATCCTT CTCAACTCCC CAACCTTTGT CCTCCCCACT CTTGCTCGC GCGGCGGTCT 180
GAGACCACCA GGACCAGTTT CAGGGGTTTC CTTCTCCAGC GAGACTTGGC AGAACAGGCT 240
TTAAAGCAA AGGAGGCAGC GGAAGACTGT GAATTCCTTT GGACAATTGA TGATATTTAT 300
CATTGTGCCC AGTTTCTACA AATAAAGAT GGGTGGATTA TTTTCTCGAT GGAGGACAAA 360
ACCTTCAACT GTAGAAGTTC TAGAAAGTAT AGATAAGGAA ATTCAAGCAT TGGAGAAGTT 420
TAGGGAAAAA AATCAGAGAT TACAAAATT ATGGGTGGA AGATTAATTC TGTATTCCTC 480
AGTTCTCTAT CTGTTAACAT GCTTAATTGT ATATTGTGG TATCTTCCTG ATGAATTTAC 540
AGCAAGACTT GCCATGACAC TCCCACATCT CGAG 574

```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

GAATTCGGCC TTCATGGCCT AGGCGCGGCC CGGGTTCCCG TTCCCCGCGG AGCCATGCGG 60
TACAACGAGA AGGAGCTGCA GGCTCTGTCC CGGCAGCCGG CCGAGATGGC GGCCGAGCTG 120
GGCATGAGGG GCCCAAGAA GGGCAGCGTG CTGAAGCGGC GGCTGGTGAA GCTGGTGGTG 180
AATTTCTCTT TCTACTTTTG GACAGACGAG GCCGAGCCCG TCGGAGCCCT GCTGCTGGAG 240

```

CGCTGCAGAG TCGTCCGGGA AGAGCCCGGC ACCTTCTCCA TCAGCTTCAT TGAGGACCCT 330
GAGAGGAAGT ATCACTTCGA GTTCAGCTCG AG 332

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAATTCGGCC TTCATGGCCT AATTGCAAGA TCACGGAATC TCCTGAATCA TTAAGAAAAG 60
ATAAAATATC ACAAGCATCT TTAGTGTTAT CTGTATTTCAG TAATTCCTTG GAGTTGTATT 120
TATTAAGCTT ACCAGATTTT AAAGGCATAT AAAATGTGGT AAGATATGAG ACACATACTG 180
AAATATCAGT GCAAAGGGAG AATGGTAGTT GAATGGTCAG AAACGAAAAA GCCTCGAG 238

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCGGCC TTCATGGCCT AGAAGCATTT TTTGTTATTG TGAACATTT TTATACTTTC 60
ATTATAATTT GTTGAGCCTA GAGTTGGGCT ATTTGAATAT TTATTATGAT AATCTTTTGG 120
CTAATGGTAA CAGCATATCT TGTTCTAACA AAATTACTGT TAACAGCAAT CGAAGTCGAG 180

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAATTCGGCC TTCATGGCCT ACTGAGATCC AGACCAGCTC CTCCCAGACC TCTCCAGAAG 60
AAGCCATGGG AACCCTCGT ATCCAGCATT TGCTGATCCT CCTGGTCCTA GGAGCCTCCC 120
TCCTGACCTC GGGCCTAGAG CTGTTTTGTC AAAAGGGTCT GTCCATGACT GTGGAAGCAG 180
ATCCAGCCAA TATGTTTAAAC TGGACCACAG AGGAAGTGGA GACTTGTGAC AAAGGGGCAC 240
TTTGCCAGGA AACCATACTA ATAATTAAAG CAGGGACTGA GACAGCCATT TTGGCCACGA 300
AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA TAACAATTGT CCAGCACTCT TCACCTCCCG 360
GCCTGATCGT GACCTCCTAC AGTAACTACT GTGAGGATTC CTTCTGTAAT GACAAAGACA 420
GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA CCACAGCTTC CACTGTGTCA ACAACCTTCC 480
ATTGTCCAAC CTGTGTGGCT TTGGGGACCT GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA 540
ATGGTACAAC TCGATGCTAT CAAGGAAAAAC CTCTCGAG 578

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTCGGCC	TTCATGGCCT	ACATGAATCC	ACTCCTGATC	CTTACCTTTG	TGGCAGCTGC	60
TCTTGCTGCC	CCCTTTGATG	ATGATGACAA	GATCGTTGGG	GGCTACAAC	GTGAGGAGAA	120
TTCTGTCCCC	TACCAGGTGT	CCCTGAATTC	TGGCTACCAC	TTCTGTGGTG	GCTCCCTCAT	180
CAACGAACAG	TGGGTGGTAT	CAGCAGGCCA	CTGCTACAAG	TCCCGCATCC	AGGTGAGACT	240
GGGAGAGCAC	AACATCGAAG	TCCTGGAGGG	GAATGAGCAG	TTCATCAATG	CAGCCAAGAT	300
CATCCGCCAC	CCCCAATCG	ACAGGAGACT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTCGGCC	TTCATGGCCT	AGGGCACCAC	TGAGTTCAGT	ACTTCAAAAT	TGCCGTGCTC	60
TACCTCTCCC	CAGTGCACAA	AAACACTCTC	CACACCAAGC	TGCTGCTGCT	GGGGGATGGA	120
GGGATGGCGT	CAGCGATTCA	AGACTGTTTT	TCCTACCTGT	TCAGCACTTC	TTTCAGCGAT	180
ATGAAGTTAA	ATCCAGTCTT	TCCCTGTCTC	CAGGCATCAT	CGCCATCAAC	ATACAGCCAT	240
ACTCCAGGAT	TGCCCCATCT	CAACATAAAC	GGACTCTCCT	GGACTCCACT	TCCCACATCA	300
GTCACAGCCA	CACTTCCTGA	GAAAGAAGTC	TACACTCTTC	ATTCACCTTC	ATTACCCAC	360
TGCTCGAG						368

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GAATTCGGCC	TTCATGGCCT	AGAGAAAATA	AAGAGTTATA	TCAGAAATTT	ACAAACATAA	60
CTTTTAAAT	TTTAAATTGC	AAAATATATA	TCATACGAAA	ATGAAAATTA	TAATCTTTCT	120
TGGATTCTTG	GGAGCCACAT	TGTCAGCCCC	ACTTATCCCA	CAGCGTCTCA	TGTCTGCCAG	180
CAATAGCAAT	GAGTTACTTC	TTAATCTTAA	TAATGGTCAA	CTTTTGCCAC	TACAACTTCA	240
GGGCCCACTT	AATTCAATGA	TTCCACCTTT	CTCTGGAATT	TTACAACAGC	AGCAGCAGGC	300
TCAAATTCCA	GGACTCTCCC	AGTTCTCTTT	ATCAGCTCTA	GACCACTTTG	CTGGACTGCT	360
CCCAAATCAG	ATACCCTTAA	CAGGAGAGGC	CAGTTTGGCC	CAAGGAGCCC	AGGCAGGCCA	420
AGTTGATCCC	TTACAGCTTC	AAACACCGCC	TCAGACACAA	CCAGGCCAC	GTCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```

GAATTCGGCC TTCATGGCCT ACTTACAGAA CCTATTCACT GGGAAGGAAG CCCTCATTAT      60
AATGATTTTC ATTCTTATGT GTGTTTCAGG ACGACTGGGT TTGGATTCAG AAGAGGATTA      120
TTATACACCA CAAAAGGTGG ATGTTCCCAA GGCCTTGATT ATTGTTGCAG TTCAATGTGG      180
CTGTGATGGG ACATTTCTGT TGACCCAGTC AGGCAAAGTG CTGGCCTGTG GACTCAATGA      240
ATTCAATAAG CTGGGTCTGA ATCAGTGCAT GTCGGGAATT ATCAACCATG AAGCATACCA      300
TGAAGTTCCC TACACAACGT CCTTTACCTT GGCCAAACAG TTGTCCTTTT ATAAGATCCG      360
TACCATTGCC CCAGGCAAGA CTCACACAGC TGCTATTGAT GAGCGAGGCC GGCTGCTGAC      420
CTTTGGCTGC AACAAAGTGTG GGCAGCTGGG CGTTGGGAAC TACAAGAAGC GTCTGGGAAT      480
CAACCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```

GAATTCGGCC TTCATGGCCT AGAAAAAGA AACTGTCGTG GATACTGTCA GTGTATATAT      60
TTATGTGGTA CCTGAGAGCC ACCCAAATT AGATTGACTT TAGATCGTTT ATACAAAAT      120
AGCTTGAAGA ACTGTTTTT CCATGGTAAA TGCTTTTGAA TATTAECTTA GTTATGTTAG      180
ATTCCTACCT CAGTGGTACT GTCACAGCCA TTGGTTACAT TTCTGAAACC CTTGAGAGTA      240
AGAGTTTTGG TTTTTGTTT TGTTTTGTG TGTTTTTGA GATGGAGTCT TGCTCTGTG      300
CCCAGGCTGG AGTGCAAGTGC AGCAACCCAG GTGGAGTGCA GTGCAACCTC CACCTCCCAG      360
GTTTAAGCGA TCCTCCTAAC CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

GAATTCGGCC TTCATGGCCT AGCTTCAGTA GCAAATAAGG ACATCATCTG CTATAACCTA      60
CAAGCAGTTG GACAGATATT CTACATTTCC TCATTCTCT ACACCGTCAA TTACATCTGG      120
TATTTGTACA CAGAGCTGAG GATGAAACAC ACCCAGAGTG GACAGAGCAC ATCTCCACTG      180
GTGATAGATT ATACTGTGCG AGTTGGTCAA ATGGCCTTTG TTTTCTCAAG CCTGATACCT      240
CTGCTATTGA TGACACCTGT ATTCTGTCTG GAAATACTA GTGAATGTTT CCAAACTTC      300

```

AGTCAGAGCC ACAAGTGTAT CTTGATGCAC TCACCACCAT CAGCCATGGC TGAACCTCCA 360
 CTTTCTGCCA ACACATCTGT CTGTAGCACA CTCGAG 395

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCGGCC TTCATGGCCT ACACCTTTCA CTTATCTTAT AGTCACTTAA TTCCTCTACT 60
 CTTATCATTT GATATTTTCA TTTTATTGTG TATCTCTGTN NGGCCAAATC AATAGATTTT 120
 GAACAATCTC ACACCTTAACC TTTTAAAAAA ATCTAATAGG CCCAGTTTCC TCTCAACAAT 180
 CTTTGAAGAA CCTTCGAGAA AGGAGAAACA CAGACCTCCC GCTTCTAGAC ATGCACACTG 240
 TAACCCGGGA AGAGGGAGAA GGCATGGAGA CAACTGATAC GGAGTCTGTG TCTTCCGCCA 300
 GCACATACAC ACAGTCTTTA GAGCAGCTGC TTAACCTCTC CGAAACTAAA CTTGGTATGT 360
 TACTCTGTCT AAATATGTTT TTCTTATTTA ATTCACTGT CTTATTTAAT TACTANTACT 420
 CTAAGTTACA TATGCTTTTT NGGGCTGCTC CAATAAAATT TCTTTCAATA TTCCACTACC 480
 TGTTTGATTT AGGTTCTCTA GAGGGACACT CGAG 514

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCT TCATGGCCTA GGTTCCTGT ACATGGAGAT TAACTGTCT TCCAAAGTGA 60
 AGAGTTTATT GTTCTAGATC TTGAGCACAA AGGTTGGTAT ACGTTAATAA AAAAAATAGC 120
 AAGGGAAGAA AATCATTTCC TTCATACCAA GTAAGAGAGC ACTTATCATG GTAGGCACCTG 180
 GCTTTGCAAT TATGAGACCA GTAGTAGAAA TAGCTTTAGT TTCTCAATT TTCTGGAGT 240
 ATTCTTCAGA CTTTCTTTAC ACTGCTCAAG GTGGGGCGAG TGGCAGGGCG GACCCTGGCG 300
 ACCTGACGCT GCGGAGGCTC GAG 323

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC TTCATGGCCT AGGAACAGTG TGTGTTTTG TGTGTGGCTT GCATTCTCTC 60
 CTCGTTTTT GGAGCAGCGT GAGATTATTG CAATGCTACA TTCTCTCCCT CTGCGCCCTC 120
 CTACCCCATC AATGTCTCAT GGGTGGTGTG ATAGAGGCTA TGGGAGTGAA GACCACTGGT 180

```

GTTAGTCTGT GTATAGTTCC TGGGGTGTGG CGAGTACCAG CTCTGACAGC GGAAGAGAAC 240
TATACTGTTG ATTCCCATTA TTCTCAGTAG GTGTGTTCTA TAAAATTGCT GCGAACACCA 300
AATTAGCGAA TCCTGAACCA TCGTTCCCAG AGGAATAGGG GGTTAGGGTC CTGTGATCCT 360
CAAGTTGCAA CATTGTCTTC GACTGATTAA TATGTAACCT TGTTTTATAT GTGCAATCTC 420
GAG 423

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

GAATTCGGCC TTCATGGCCT ACCGAAACCA AATAATTCAA GCACTGCTTA TTACAATTTT 60
ACTGGGTCTC TATTTTACCC TCCTACAAGC CTCAGAGTAC TTCGAGTCTC CCTTCACCCT 120
CGAG 124

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

GAATTCGGCC TTCATGGCCT ACATCTATGA CTTTTTAAAC ATGCGGCGTT TTGTGAATAT 60
CATGATAATA ACAAGAGTCA ACAGGCTAAG TGAGAGGAGA GGGATGCTAC GCCTACGCTG 120
CCCCCACCAC GGCCAGCCGG CTTCTGCGCC TTTGGTGTG GATTTTCTTT GTGATTTTAC 180
GGGGTTTTGT GTTTTTTTTT TCTTGTTTTT TGTTTTGTTA TTTTTCCTTG TCCACTTGAT 240
TTGCATGCAA CACCACAAA AAGGAAACAC AAAACCCCGT CTGCTCGAG 289

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

GAATTCGGCC TTCATGGCCT AACTATGAG AGGACCGATT GTATTGCACA TTGTCTGGC 60
TTTCTGTAGC CTTCTGCTTT TTCAGCGTTG CCACACAATG TCTGGCCTTC CCCAAAATAG 120
AAAGGAGGAG GGAGATAGCA CATGTTTCATG CGGAAAAAGG GCAGTCCGAT AAGATGAACA 180
CCGATGACCT AGAAAATAGC TCTGTTACCT CAAAGCAGAC TCCCCAACTG GTGGTCTCTG 240
AAGATCCAAT GATGATGTCA GCAGTACCAT CGGCAACATC ATTAAATAAA GCAAACTCG 300
AG 302

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```
GAATTCGGCC AAAGAGGCCT ATTTT TTTT CTGCAAACAC TGTGTATAGT GAGACTTGT 60
CTACTTTGGA GAACAGGTTA CCTTTTGAAA ATGAGGTTGA GTTCTTCCT TTCTGATGCA 120
TTGATTTTGG AAGATTTT TTTCCCCTT CCCCTCTCCC TCGAG 165
```

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```
GAATTCGGCC AAAGAGGCCT AGCTTCTTG TATAATTAAA TCTGAGTTT GTTGAGCAT 60
CTTCAACAT GTACCATATT TATGACAATT CTCTCCATA GGATCTATCT GTTCTGCAAC 120
AAGTATTGAT CTTACAGTAA AATTTTTCAC AAATTCATTA GATTCTATGT CTCTTTTCT 180
GGTAGGAATT TTTGTGCAGG TAGCTATCTC TTGCCCTAGA TTATTCTCCT TGTTTAGCTG 240
CTGATTCTTA AACTGGCCTC TAGATTTCCT GATTCTTCC GGTACAGACT TTCTCTTGC 300
AAGTTCTTCC ATCTCTAATC TTTGAGATTA ATCTTCTTTT GAAATGTCCT GCTGCTCTAC 360
TCTTGATGTT CTCGAG 376
```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```
TCTCCAAGGG AAAATAAATG CTTTACTAT CTAGTTTGTC TCTTGAGAA TTAAACTCT 60
TTTTTTTTT TTTCAATCCA GTAGCTTTTG GGGTAGAGTT TGGCTCTTTG AGAATTGCAT 120
ACTAATTAAT TTTAGGGGTG ATTTGTACAT CATCTCTATA TTCCTGAAAC ACAGTAGAAA 180
CAGCCAGCAG TCAGGCAACC ATCTACCATG ACCATTAAAA CATCCCCAAA GTGAAACACC 240
AGATGTGATC TGCTAGATTT AGTGAGGCG GCTGGCTCGA G 281
```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```
GAATTCGGCC AAAGAGGCCT AGCTAGNCTT GCTCAGCTTT GTGGATACGC GGACTTTGTT      60
GCTGCTTGCA GTAACCTTAT GCCTAGCAAC ATGCCAATCT TTACAAGAGG AACTGTAAG      120
AAAGGGCCCA NCCGGAGATA GAGGACCACG TGGAGAAAGG GTCCACCAG GCCCCCCAGG      180
CAGAGATGGT GAAGATGGTC CCACAGGCCN TCCTGGTCCA NNTGGTCNTC NTGGCCCCCN      240
TGGTCTCGGT GGGAACCTTG CTGCTCAGTA TGACGGAATA GGAGTTGGAC TTGGCCCTGG      300
ACCAATGGGC TTAATGGGAC CTAGAGGCCC ACCTGGTGCA GCTGGAGCCC CAGGCCCTCA      360
AGGTTTCCAA GGACCTGCTG GTGAGCCTGG TGAACCTGGT CAAACTGGTC CTGCAGGTGC      420
TCGTGGTCCA GCTGGCCCTC CTGGCAAGGC TGGTGAAGAT GGTCAACCTG GAAAACCCGG      480
ACGACCTGGT GAGAGAGGAG TTGTTGGACC ACAGGGTGCT CGTGGTTTCC CTGGAACCTC      540
TGGACTTCCT GGCTTCAAAG GCAACCTCGA G
```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```
GAATTCGGCC AAAGAGGCCT ATGCGCAAGG ATCAAGCCGA CTACCTGTGC TGTCTACTGG      60
GACAGCAGTC TCCGAGCTAC TCCGTACCTC CCTCTGCCAG GTCGTGGAGT TAGGCCCCAG      120
TCCCTACTTG TCACTGGTTC CCACTGTGCT CTAACCTGTG CAGCACCTGG GAGCTCTGGC      180
CTGGGGCTGG AGGCCCTGGT AGGAGCTGCA GTTGGAGGCC GTTCTGTGCC CAGCAGCGGT      240
GAGCGGCTCC CATGGGCCCT GTGTCTGCAG GGAGCCAGGG CTGCGGCACA TGTGCTGTGA      300
AACTGGCACC CACCTGGCGT GCTGCTGCCG CCACTTGCTT CCTGCAGCAC CTCCTACCCT      360
GCTCCGTGTC CTCCTCTCC CCGCGCCTGG CTCAGGAGTG CTGGAAGAGC TCACGCCTCG      420
GCCTGGGAGC CTGGCCTCTT GATATACCTC GAG
```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```
GAATTCGGCC AAAGAGGCCT ATGTCATGAG TGAACCTGGC AATTGCCTTG TTAAGACCAG      60
TTGGACATTA TCTTCCACAT TGCGAAGCTA TACATGTCTG ATATGTTCTG AAAGAATAGA      120
ATTTATAGTT AGATATACTA TTTTGTGATTA TTTACTCAGA AGGAGACATG TAATTATTCT      180
TATGTTGTCA TGAAATCTA TTAAATGCAT TTATATTTCAT CATCAATGTT ACGAAGTTCC      240
ATTATTATTA TTTTACAGAG GGAAGCCAA GATACAGGAG TGAAGATTAC TTGGCCTATC      300
GCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

GAATTCGGCC AAAGAGGCCT AAGAAGATGA ACAAGCGCCA GCTCTATTAC CAGGTTTAA      60
ACTTTCGCCA TGATCGTGTC TTCTGCACTC ATGATATGGA AAGGCTTGAT CGTGCTCACA      120
GGCAGTGAGA GCGGCATCGT GGTGGTGCTG AGTGGCAGTA TGGAGCCGGC CTTTCACAGA      180
GGAGACCTCC TGTTCTCAC AAATTTCCGG GAAGACCCAA TCAGAGCTGG TGAAATAGTT      240
GTTTTTAAAG TTGAAGGACG AGACATTCCA ATAGTTCACA GAGTAATCAA AGTTCATGAA      300
AAAGATAATG GAGACATCAA ATTTCTGACT AAAGGAGATA ATAATGAAGT TGCTCTCGAG      360

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

GAATTCGGCC AAAGGGGCCT ACCTGAAACG GCAGTCCGGT CCCTCCGACA TTGTCCAGCG      60
GAAGGCCTGG GCTTCACACT CTGTGCCTCC CGGCGCTACC TGGCAGGATG CCGAGCACAC      120
AGCAGATGCT CAATGAATGC CCAACCAACC CTATACCTGG CTTGGATCTC AAGCTCCCTG      180
GCCGGGGCCT GATGGAAGGC TTTGGGGGCA CAGGAGGCTG CCCCTTGGG CGCCCCGGGC      240
CACCTCTTCG CCCTCGAATC TCAGGCAGCT TGGTCAGGAA CTTCTTCTCC ACGTATTTAG      300
CGTGAATCCA GGCCTCCTTC TCCTGCCTGT GGGAGGGGAG AAGCACGCAG TCTTCCCTCT      360
TCTGCTCCAG GGGTCCCCCA TTCCCTGGG AGGCTAAACC CATAGCTCGA G              411

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

GAATTCGGCC AAAGAGGCCT AGGGAGTGTT TGGGTTTCTT CTCCGTTTGG CAGTGAAACA      60
CATCTCAGAA AGGTGGAGCT GATCAGAATA ATGTTTCAGCA TCAACCCCTT GGAGAACCTG      120
AAGGTGTACA TCAGCAGTCG GCCTCCCTCG GTGGTCTTCA TGATCAGCGT AAGCGCCATG      180
GCCATAGCTT TCCTGACCCT GGGCTACTTC TTCAAAATCA AGGAGATTAA ATCCCCAGAA      240
ATGGCAGAGG ATTGGAATAC TTTTCTGCTA CGGTTCAATG ATTTGGACTT GTGTGTATCA      300
GAGAATGAAA CCCTCAAGCT CGAG              324

```

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```
GAATTCGGCC AAAGAGGCCT AGTGGGGCTG TATTTTAATA CAAGAAAGAC ATTGCTCTAG      60
AACATGGCTC GCCTTTGCTT CAGGGCCTAG CAGTTTATTT TAGCCATAAG GGTAAAGGAG      120
CAGGTCAGAA ATGACTTTTA GTGTAATCCT ATCTGTAATT AAAAATACAA ATGCTGTCAT      180
AAGATCAAAAT GTTATCAAAA ATCAGTATTT AAAATTAAAT TTACCCCCAA ATTTCTTTCA      240
AAAAAGTTGT AATGTTCTTT TTCAGTGAAG CCTTTGCACT GCTAGAGCTG AAGAATGTGA      300
TCAATCGGCT TGTGAATAA TCCCGCACAG TAGGTATTCC GCTGAAGCCA ACTCTAGCTG      360
GGGGCTCGAG                                     370
```

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```
GAATTCGGCC AAAGAGGCCT AAGAAATAGG ACTATACAAA TTTTCAACTT CTTTGTATAT      60
CAGTTTGGT AAGATGCATT TTTCTTCTGA GAATTTGTTT CATTTGAATT TCCAAATTTA      120
TTAGCATGAA GTTGTAAATA AAAATCTTAT ATTTTACTC AAATTTTGAG ATAGTTGTAG      180
ATTTACATGA AGTTGTAAAG AATAATAGAA AGATCCTGTG TACCTTTTCC CAGTTTCCC      240
CAAAAGTAAC ATTTTGCATA ACTCTAGTAC AGTAGCACAA CTCGAG                                     286
```

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```
GAATTCGGCC AAAGAGGCCT AGGCAAACCG TGTACTAAGC ATCAGTGCAG AGATAGTGAA      60
TGAGACACAG TATTCACCAC TTGAGCAGT GCCAGTCTAG TATTAGAATA TTTTGGCTA      120
AAAAATTATT TTGAAGCATA AAGAAGCTTT TGTTTGCTCT GGTGATTTTC ATAACATATT      180
CACATTCTTA ATGTATTTT GGTTTTTCAG AAAGTTACTT CTGGCCTGTG TTCTTTCAGA      240
ATATAGGTTG CAGCTTGTGT TAAGTGCAGG AACTATTGAT AGACTGAGTT TAGAAGAAGG      300
GAAACTCGAG                                     310
```

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCGGCC AAAGAGGCCT AGGACTTTGG GGCAGGTGAT TAAATTTATA TAGGTACCTC	60
AAGAAAAAGA ACCTGAATAT GCTGCATTTT CTTTCTTTAG CTTTACATG TAGCATTTTG	120
TTTGTCTTTT GTTATTTTGG TTTTGATATA TGCTTTTGG ACCCCAATAG ACTGTTGAAA	180
GAAATTTAAA AATTACTCTT STAGGGATAT AGTATCCTTA AAAAAATAAA ATTAAAAAAA	240
ATTTAAAAAA ATTGCTGCAA TATCTGGCTC GAAGGTTGCC CTATATTAGA ATAATACTTT	300
AGCCAAACAC ATCAGCTCGA G	321

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCGGCC TTCATGGCCT TGTGATTCTG CAAAGGAGGA ACAATAATTC ACTGTTTCCC	60
AAACTTATCT GACCATAGAA CATATNTCTC AGAGTATTTT TCAAGAGTAG TATTTTCTGT	120
AATATATGAT GAAAAATAAT CGTATCGGCC ATCTTTGTAC ATAAGGTCAA AATGTCAGCC	180
AGCCCTGAAA TAAATGCAAG CCAAAAGGTA GAGAGATAAG TGAATAAAGC TGGCACACTG	240
TCAGTCCGGA GTACCATGCT GCATTCTGAG TCAAGCTCCA GGAAACTGAG CTAGGGTTTG	300
TCTCTAAGAA GAAAAACTGG AGCGTCCAAA GCTTCTGGAT TCCATTTAAT TAAAACCTTT	360
TTAAATTAAA TCCTTGTAAC TGAAGAGTAT CGGTGGATGA AGAAAAAATA GTCTCACATG	420
TCTTCATTTC CATCCTTGGC TCAGTACAGC TCCAGTTCCA TTATTCTTAA ACATCTATTA	480
ACATGATTGC TAAATAATTA CACAGGCTAA CTGCCAAGCA TTTTTCACAG GAAGCAAGGC	540
ACTGCTCGAG	550

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC TTCATGGCCT AGTTAAGTGG GAAGTTAAAT GGCAAGTACT AGAATGCCAC	60
CTATGGCAAG CACTAGAATG GTCTAGGTGT GAAATGAGGG AGTAATGTCA GGGAGTCAAG	120
GTGGCCATCC ATAGCAGTGA TTCTTATCTG GGGTAGGGGG TGAATTTTCA GTGGAGGGAG	180
GTCTCTGGAC ATGGACCCCC AGGCAGGGCT ATCCAATCAT CTGAGGGGTG AGCAGTGTTC	240
AGCTCAGTAA AAGTAAGGGA AAAAAAATAG CAGTCTCTAA AAGGAACATA GAGCGCTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

GGGGAGAGCA TCAGGAAGAA CAGCTAATGG ATGCTGGGCT TAATACCTAG GTGATGGGAT      60
GGTCTGTGCG GCAAACACCA TGGCACAAGT TTACCTATGT AACCTGCACA TCCTGACATG      120
TACCCCTGAA CTAAAAATGA AAGTTGGAGA CCAAAAAACA AAACACCATA AAATACAAA      180
ACTTCTTAAA CAATAAACTA GTAGAAAATT TCTAAAATAT ATAATTCAAG AATTATATAA      240
GAGCTCTTTT TATATGTAAA TATAAATTTA AATACAAGAG AAACATCTAA AACAGGTTGC      300
TTCTGAGAAA CGTGACTGGT TATTAAGAAG AGGTATATAG GGCCTCACTC GAG              353

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

CATTATTTAA CCTTTTAAAC AATCAAGAGA TTGCTTTTAA AATTGTCTCT AAAAAGGTTT      60
GATTTTTTAC GAAAGAGAGA GCACTTGAAT ATATCTTTAT GTACCACCGT GTCTCTTTT      120
GTTAGATTTT TCATCTGTGG GTATAATATA AAATATTCTT AAAATGAAAG CTTTACGCTT      180
GTGTTTGAGA CTAAGCAACT TGCATTGTGT CATGACCCTT CTAATACCAC AAACCCTCGA      240
G                                          241

```

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```

GAATTCGGCT TCATGGCCTA CACTCAACCA CTGAAAAAGC TGAAAATCAA TGTTTTTAAG      60
GTTCAACAAGT GTGCCGTGTG TGGCTTCACC ACCGAAAACC TGCTGCAATT CCACGAACAC      120
ATCCCTCAGC ACAAATCGGA TGGTTCTTCC TACCACTGCC GGGAGTGTGG CCTCTGCTAC      180
ACGTCTCAGC TCTCTCTGTC CAGGCACCTC TTCATCGTAC ACAAGTTAAA GGAACCTCAG      240
CCAGTGTCCA AGCAAAATGG GGCTGGGGAA GATAACCAAC AGGAGAACAA ACCCAGCCAC      300
GAGGATGAAT CCCCTGATGG CCCCTCGAG              330

```

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GCGGGCACCA	TTCCAGTAT	GTACCAAACC	AAAGCCGTCA	TCATTGCAAT	GATCATCACT	60
GCGGTGGTAT	CCATTTTCAGT	CACCATCTTC	TGCTTTCAGA	CCAAGGTGGA	CTTCACCTCG	120
TGCACAGGCC	TCTTCTGTGT	CCTGGGAATT	GTGCTCCTGG	TGACTGGGAT	TGTCACTAGC	180
ATTGTGCTCT	ACTTCCAATA	CGTTTACTGG	CTCCACATGC	TCTATGCTGC	TCTGGGGGCC	240
ATTTGTTTCA	CCCTGTTCTT	GGCTTACGAC	ACACAGCTGG	TCCCGGGGAA	CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GCCAGACTAC	CACAAGCCCC	ACCCACACTA	TGCCAAGCCC	TACCCATACC	ACAGCAAGCC	60
CCACTCATAC	TTCCACAAGC	CCCACCCATA	CCCCCACAAG	TCCCACCCAC	AAAACCACTA	120
TGTCACCTCC	CACCACTACA	AGTCCTACCC	CCAGTGGTAT	GGGCCTAGTC	CAGACTGCCA	180
CAAGTCCAC	CCATCCTACC	ACAAGCCCCA	CCCATCCAC	CACAAGCCCC	ATCGTTATAA	240
ATGTAAGCCC	TTCCACTTCT	CTAGAACTTG	CTACCCCTCT	CAGCCCTCTC	AAACACTCAG	300
ACCCACCCCT	CCCAGGCAAT	GACTCCCTTC	CCTGTAGTCC	CCCAGTCTCC	GATTCTCTACA	360
CTCAGGCAGA	CCCTATGGCC	CCCAGAACTC	CCCACCCAAG	TCTCGAG		407

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ACTGAGCTCA	AGGACCCCTC	CAAGAAGAAG	ATGCAGCACA	TCTCCAACCT	GTCCATCGCT	60
GTCATGTACA	TCATGTACTT	CCTGGCTGCC	CTCTCGGCT	ACCTCACCTT	CTACAACGGG	120
GTGGAGTCGG	AGCTGCTGCA	CACCTACAGC	AAGGTGGACC	CGTTTGACGT	CCTGATCCTG	180
TGTGTGCGCG	TGGCCGTGCT	GACAGCAGTC	ACGCTCAGAG	TGCCCCATCGT	TCTGTTCCCC	240
GTGCGCCGCG	CCATCCAGCA	GATGCTGTTT	CCAAACCAGG	AGCTCGAG		288

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

GAATTCGGCC TTCATGGCCT AGTCAAGCTA GGTAAGCTAA AAAGAAGAAA ACCTGGTTAC      60
AGCCCCGGTGA ATTGATTTTT TTCCAGCCGA GAAATAGATA TTTCTCTCAC ATATATTGG      120
AAAACTTTAG TCATCTTCAT AAAACTTAAA AAGTTACCTA AGCACACACA GCAAGTTTCT      180
CCTTTCTTCC TTTTCCACAC CCTTACCAGT TCACTATGTT TCTACCAATC CAGTGCCCGAG      240
TTGCCAATGA TGTTGCTCTC ACATGAATT ACTGCATTCC CTTCTGGTTC CCCAGAAGGT      300
CTTGAAGAAA GAGGTTGAGA CTAGTGGACC CAAACAGAAT TTCTTGGCTG GTGATACTCA      360
GATTGTGTTT AGAGCCTGGT ATGAAGAAGG GGCCAGGTGT AAGAAGTAGT TAATCAACTG      420
CACGTTGATT TCAGGCTGAA TATTCAACCA TCTGCAGCCA CCCGTCTCTA AAAGTCTAGC      480
TGAAGCACAA TTGATTGTGC CATAGAATGA GCAAACGCTT GAAAACACAA GCTCGAG      537

```

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```

GCGAGCTCGT GTTTTAAAGG ACCAAATAGA AGTTTACCAG GAGAGAAGTG ACAGAAGTGC      60
TGCTAGATA GAGGAAGGGC ACACACAGAT GCAAGCATGT GCAGAAATGA GCAAACCACT      120
GAGACGCTGC CTTGAGCTCT GTGTCACACT GCTATGTTGC AGCCTGGGAG GCTGTTCCTCA      180
GTTGAGCCCT TCGGAACCAG CCATGAGATG GCACGGGTAC GCGGAAGGGA GCAGTCTCCA      240
TGGCTGGGTG GTGATGGGGG CTTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

GATGGCTCCC CAGAGCCTGC CTTTCTCTAG GATGGCTCCT CTGGGCATGC TGCTTGGGCT      60
GCTGATGGCC GCCTGCTTCA CCTTCTGCCT CAGTCATCAG AACCTGAAGG AGTTTGCCCT      120
GACCAACCCA GAGAAGAGCA GCACCAAAGA AACGGAGAGA AAAGAAACCA AAGCCGAGGA      180
GGAGCTGGAT GCCGAAGTCC TGGAGGTGTT CCACCCGACG CATGAGTGGC AGGCCCTTCA      240
GCCAGGGCAG GCTGTCCCTG CAGGATCCCA CGTACGGCTG AATCTTCAGA CTGGGGAAAG      300
AGAGGCAAAA CTCCAATATG AGGACAAGTT CCGAAATAAT TTGAAAGGCA AAAAGCTCGA      360
G

```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

GCCACAATAG CGGGATTGAT CTCCTTAGGA CCTATCTTTG GCGTTGCCAG TTCCTTTTAC      60
CTTTTGTGAG TTTAGGTTTG ATGTGCTTTG GGGCTTTGAT CGGACTTTGT GCTTGCAITTT    120
GCCGAAGCTT ATATCCCACC ATTGCCACGG GCATTCTCCA TCTCCTTGCA GGTCTGTGTA      180
CACTGGGCTC AGTAAGTTGT TATGTTGCTG GAATTGAACT ACTCCACCAG AACTAGAGC      240
TCCCTGACAA TGTATCCGGT GAATTGGAT GGTCTTCTG CCTGGCAGAA CTCGAG          296

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

GAATTCGCC TTCATGGCCT AGGATGTAGA ATCCTGCTTA TCTGTGAAAT GCAGTTGACA      60
CATCAGCTGG ACCTATTTC CGAATGCAGG GTAACCCCTC TGTTATTTAA AGATGTAAAA      120
AATGCGGGAG ACTTGAGAAG AAAGGCCATG GAAGGCACCA TCGATGGATC ACTGATAAAT      180
CCTACAGTGA TTGTTGATCC ATTTCAAGATA CTTGTGGCAG CAAACAAAGC AGTTCACCTC      240
TACAAACTGG GAACAATGAA GACAATGAAC TCGAG          275

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

TCGTTCCCTT CATCTCTTCC CTGCCCAGAG CAGGGACTCT CTCCATATAA ACAAAGGAA      60
AACCACTGGC CAGGGTATGG TCAATACCTC AACATATCCA GACATCACAG CACCAGAACA      120
CCAGTATGTA TATTCCACAA GTACTCGAG          149

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

GCAATCAGAT AAAGAAAGAC CTGGCTGACA AGGAGACACT GGAGAACATG ATGCAGAGAC      60
ACGAGGAGGA GGCCCATGAG AAGGGCAAAA TTCTCAGCGA ACAGAAGGCG ATGATCAATG      120
CTATGGATTG CAAGATCAGA TCCCTGGAAC AGAGGATTGT GGAAGTGTCT GAAGCCAATA      180
AACTTGCAGC AAATAGCAGT CTTTTACCC AAAGGAACAT GAAGGCCCAA GAAGAGATGA      240

```

TTTCTGAACT CGAG

254

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GACAGCCTGG AAGTTGGAG ACCCTGACAC ACCCACCTTC TCACCTGGGC TCTGCGTATC	60
CCCCAGCCTT GAGGGAAGAT GAAGCCTAAA CTGATGTACC AGGAGCTGAA GGTGCCTGCA	120
GAGGAGCCCG CCAATGAGCT GCCCATGAAT GAGATTGAGG CGTGAAGGC TGGGAAAAG	180
AAAGCCCGCT GGGTCCTGCT GGTCTCATC CTGGCGGTTG TGGGCTTCGG AGCCCTGATG	240
ACTCAGCTGT TTCTATGGGA ATACGGCGAC TTGCATCTCT TTGGGCCCAA CCAGCGCCCA	300
GCCCCCTGCT ATGACCCCTG CCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GCCTGGAACC TGATTCTCCT GACCGTCTTT ACCCTGTCCA TGGCCTACCT CACTGGGATG	60
CTGTCCAGCT ACTACAACAC CACCTCCGTG CTGCTGTGCC TGGGCATCAC GGCCCTTGTC	120
TGCCTCTCAG TCACCGTCTT CAGCTTCCAG ACCAAGTTCC ACTTCACCTC CTGCCAGGGC	180
GTGCTCTTCG TGCTTCTCAT GACTCTTTTC TTCAGCGGAC TCATCCTGGC CATCCTCCTA	240
CCCTTCCAAT ATGTGCCCTG GCTCCATGCA GTTTATGCAG CACTGGGAGC GGGTGTATTT	300
ACATTGTTCC TGGCACTTGA CACCCAGTTG CTGATGGGTA ACCGACGCCC GCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GCGGGCTGCA GAATGATAGA CGAGCTCAAC AAAACGCTGG CCATGACCAT GCAGAGGCTG	60
GAAAGCTCTG AGCAGCGGGT CCCCTGTTCC ACTTCTTACC ACAGCTCTGG GTTGCACTCG	120
GGTGATGGGG TCACCAAAGC AGGACCTATG GGCCTTCCAG AAATAAGACA AGTGCCAAC	180
GTGTGATTG AATGTGATGA CAATAAGAA AATGTGCCTC ATGAGTCAGA CTACGAAGAC	240
TCTTCTTGCC TGTATACAAG AGAAGAGGAG GAAGAGGAGG AGGACGAAGA CGACGACGAA	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

AATCAATCAA CTAGGCATAT GACACAGTAG TCCATTATAA AAGAAGACAT ACATCCAGCA      60
CCATCAACTA ATTCTTAAGA TAAGTTATCT GGGAAAATTG AAGAACAAAT AAATTCACAG      120
AAATACTGTA AAGTGAACGA AGACATAAAA CCAAAGAAAA CTGAGGCCAT TTCTGCCAAG      180
AAAGGAACAG CAAAGAGTAA AGATGAAAAA TATTCTAAGA TAATACCAGA AAAAGATAAT      240
TCCTACATGG ACAAAGATGA GCATGGTTCA TCCTCTGAAA GTGAAGATGA AGCGCTGGGT      300
AAATATCATG AGGCCTTATC CAGAACACAC AATTCCGGAC TACCACTCGA G              351

```

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```

AAGTTAAAGG TATTAAATAA ATGAGTTTCT CCTTAATTTT GTTAATGCTC TTTTAGCTAA      60
TAAGACTTTT TCTAGAGTTA CATATTTTAA TCTGTTTCAT TTTTATTTT TCCTTTGGTT      120
TTATATTTT AAAAGCCATT ATATCCCTCC CACTGGTAAC ATACACATAC ACAGACACAC      180
ATCTATTTC AATGAATACT TACTACTTTA TCATTTTCAG TCTTAATTGT ACT              233

```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

CGCGCGCCGC AGCAGTTCCA GGAAGGATGT TACCTTTGAC GATGACAGTG TTAATCCTGC      60
TGCTGCTCCC CACGGGTCAG GCTGCCCAA AGGATGGAGT CACAAGGCCA GAATCTGAAG      120
TGCAGCATCA GCTCCTGCCC AACCCCTTCC AGCCAGGCCA GGAGCAGCTC GGACTTCTGC      180
AGAGCTACCT AAAGGGACTA GGAAGGACAG AAGTGCAACT GGAGCATCTG AGCCGGGAGC      240
AGGTTCTCCT CTACCTCTTT GCCCTCCATG ACTATGACCA GAGTGGACAG CTGGATGGCC      300
TGGAGCTGCT GTCCATGTTG ACAGCTGCTC TGGCCCCTGG AGCTGCCAAC TCTCCTACCA      360
CCAACCGGT GATCTTGATA GTGGACAAAG TGCTCGAG              398

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
GAATTCGGCC TTCATGGCCT ACACCCAGCC AATTTTTTTG TATTTTITAGT AGAGACGGGG      60
TTTCACCATG TTAGCCAGGA TGGTCTCTAT CTCCTGACCT CATGATTGTC CCGCCTCGGC      120
CTCCAAAAAA AGAACATTTT ATATTTGAGT GCTATTCTTT TTGCGGCACC AAAACTTTAT      180
AACACACTGC CTTCTGAATT TTTTTTTTGT GTTCTGCTC AGCTCATGT TAATCATATT      240
GTTCCCATGT ATGTCATGAG TTATTTTCTT CCTAGTCTTT TCAAAATTTT CTTGTCTTTG      300
ACTTTTAACA GTTTAATTGT AACAGTGTAT ATCTTTAAAG TTAAATTCAT GCTTGTGAAT      360
TTTTATAAGA GCCACAAAGG CCTTCCTCTG TGTTTTGTGT TTGTTTTTGT TTTTGTTTTC      420
ATTTTGAAGA CAGGCTCTCA CTGTCCTCTA GTGGCTCTCG AG                        462
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
TGGACAGTCT AGAAGATGCT GTGGTGCCCC GGGCTCTGTA TGAGGAGCTG CTGCGCAACT      60
ACCAGCAGCA ACAGGAAGAG ATGCGCCACC TCCAGCAGGA GCTGGAGCGG ACTCGGAGGC      120
AGCTGGTACA ACAGGCCAAG AAGCTCAAGG AGTACGGGGC ACTTGTGTCT GAAATGAAGG      180
AGTCCCGTGA CCTTAACCGG AGGCTCCAGG ACGTGCTGCT CCTGAGGCTT GGCAGCGGTC      240
CCGCCATTGA TCTGAAAAAA GTAAAGTCAG AATGTCTCGA G                        281
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
AATGGAAGTG CTGACACAAT ACTCGTGTA CTGTGTGGAA CCGCATAATC CCAGCAATGG      60
CACATTGAAG GAATGGAGGG AATCCAATAT TTCTGCCTCT GACATAATTT GGGAGAACCT      120
AACTGTGTCA GAATGCAAT CATGTCATGG AGAGTATGTT GGACGGGCCT GTGGCCATGA      180
TCACCCATAT GTTCCAGATG TTCTATTTTG GTCTGTGATC CTGTTCTTTT CCACAGTTAC      240
TCTGTCAGCC ACCCTGAAGC AGTTCAAGAC TAGCAGATAT TTTCCAACCA AGGTTTCGATC      300
CATAGTGAGT GACTTTGCTG TCTTTCTTAC AATTCTGTGT ATGGTTTAA TTGACTATGC      360
CATTGGGATC CCATCTCCAA AACTACAAGT ACCAAGTGTT TTCAAGCCCA CTAGGCTCGA      420
G                                421
```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

AAGCCAATGG CTGGTCGTGA TCCTGAATGC CACGACAG AAATGATTAA GAAAGAAGAA      60
GAACGTTTGA GGGCTTCCAT ACGTAGGGAA TCTCAGCAGC GCCGAATGAG AGAGAAACAG      120
CACCAGCGGG GGCTGAGCGC CAGTTACCTG GAACCTGATC GATACGATGA GGAGGAGGAA      180
GGCGAGGAGT CCATCAGCTT GGCTGCCATT AAAAACCGAT ATAAAGGGGG CATTGAGAG      240
GAACGAGCCA GAATCTATTC ATCAGACAGT GATGAGGGAT CAGAAGAAGA TAAAGCTCAA      300
AGATTACTCA AAGCAAAGAA ACTTACCAGT GATGAGGTAA GACCAAATTT ATTCAATTCT      360
AGGGGTTTAT CCTGTAATCA GGAGCCAAC TCTTGAATG AAAAGCTCAC ACTCGAG      417

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

CAAGCATACA ATCAACTCCA AGCTCGGTAT CACCTGAGCC CAGGAAGTGG AGGCTGCAGT      60
GAGCTATGAT CAGTAAACCA CAAGACAGGT TCACTGGCTC CCATCCCAAC CCGGACCAGC      120
TCCCTAGTAT AACAACTCAC ATGCATGTGG ACTATACCCT TACAGCCTTC TTCTGTGTGT      180
TTATGTGCAT ATATGTAGCC ATAGGAAAAA AAATCAAAAT CCTTTGGTGT TCTTTCTTAT      240
TTTTTCAAAT ATTACCTG CCCCATTCTC TTTCTTTCT CCTTCTAGTA CTCCATTGC      300
ATGCAGTTCT CGAG                                     314

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

GTGTATGTGG GGGGTAAGTG TGTGTGTGTG CGTGTGCGTG TATGTGCACG TGTGTGTGT      60
GTGCGCCTGC ACACGGAGAG CCCACTCATA CGTAGCAGAA AATCAAATGG CCCCAAATCA      120
GAAACATGGC GCATGTGAGC ATGCCACTTC TTGTGTGCCT GTGACTGTTT AGAATGTACA      180
CGGCCCTGCA GCTCCGAAG GCCAGCTCTG CTGCAACCCC TCCTCTGTCC AACACAGTCC      240
TCACTGGTGT CTTTCTCTCT TCAAATCTAC AGCATTTCTG ATCTCTGCAA ACAATTAAAC      300
CCAAAACCAA GTTCTGGCTG ACAAGGCTAC ATCTTGTTC TTGTGCGTGA TTAGCCTGGA      360
G

```

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

GCGATTGAAT TCTAGACCTG CCTCGAGTCG ATGCACCGAA AAGGGTGAAG TAGAGAAATA      60
AAGTCTCCCC GCTGAACTAC TATGAGGTCA GAAGCCTTGC TGCTATATT CACACTGCTA      120
CACTTTGCTG GGGCTGTTT CCCAGAAGAT TCTGAGCCAA TCAGTATTTC GCATGGCAAC      180
TATACAAAAC AGTATCCGGT GTTTGTGGGC CACAAGCCAG GACGGAACAC ACTCGAG       237

```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

GAATTCGGCC TTCATGGCCT ACTTTATTTT TTAAATTATT ATTAGTATTA TTTTGAGACT      60
GAGTCTTGCT CTATCACCCA GGCTGGAGTG CAGTGAGCTG AGACTATGCC ACCGCACTCC      120
AGCCCGGGCG ACAGAACGAG ACTCCATCTC NAAAAAAAAA AAAAAAATCT ATGTTTCATGC      180
CTTNACACCT GTTCTGCAC ATAGCTGTGC AGTATATTCT TCTTCTAAGC AACGACCCAG      240
TGAAGATCCA AACAAAAGTT CACAAATATG TAGTTATCCA AGGCACCTCG AG              292

```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```

GAATTCGGCC TTCATGGCCT ACAATCTTTT AACTTTGGGG GTCACAGTTT TAGCCACCTT      60
TCGGGGGGTG ACTGGAGCAG TAGGAGGTGT GGGGTCATTT TATGAATATA ATAAATGGA      120
GCTGACTGTA CTCGAG                                     136

```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

GAATTCGGCN TTCATGGCCT AAAATAACAC ACAATTAGTA TAGAAAAAATT GCAAACACAG      60
ATAAAAGTCC TTTCCCTGTG AATTTCGTAA TGCACCTTTG AATATTCACA TCTTACTGCC      120
AAAATGAGAT TGTCTTGTGT GCCGTTCTGG AATTGCTTT TTTCCAGCTT ACATGTTCTA      180
GGTCCTTCCA GATCAATAGC TGCACCTCCCT CCTTCCTCTG CTGGTTTCTC AGCTCGATGG      240
GCTGTAAGTG GCATTACTCT CGAG                                         264

```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

GAATTCGGCC TTCATGGCCT ACAACCTCAT AAATCTCATT CTTAATTTCA CTCTAGGACA      60
GAATTATGT AGCACCTGTG TTCTGTTATT TTAGATTCAT TTTAACTTAC CTAGACACGG      120
GTACTGTGGT AGTTGTAGAG GTACAGATGT TGAGTTCCCA TCCTCCTGGC TTAATGTCAC      180
TGGGGTTATT AATACTTTC ATAAGCATTT TAGGGACACC TGCTGTCTGC TCAACCCCA      240
GCAAACCTCGA G                                         251

```

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

GAATTCGGCC TTCATGGCCT ACATCTGGTA AATTTTCTT TCTGCCTGAG GAACACCCTT      60
TAGCATTTAT TTAGTCTGCT GGTGACCAAT TCTCATATTT TGTGTTGCTG AAAAATACCT      120
TTATTTTGTT TTAATTCCTG AAAGATATTT GCAGTGGTGT GATTGGATTG ATGATTGCTT      180
ATTATTTTCT TTTTCTTTT TCTTTTGA GACAGAGTCT CGCTGTGCGC CAGGCAGGAG      240
TGCACTGGCC CGTACTCGAG                                         260

```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

GCTCTGAATC TATTTTCTAG GACATTTTTC TCCCATTTAG ATTAAGCCAG AGAGAGCCCT      60
TTCTTGCCTC CCAAGAGTTT TTCTTTGTGT GACTGTTGGT ATTCTGAACC TCTTGGATT      120

```

GATGCCTGGA ATTGTCCTAG AGACTCTCCT GATTTCGTGTC TCATTCTTTG ATTTACCCTT 180
 GGGGAGCTGG GGAAGAGATA CCTTCCCATG GCATCACTTG TTAAGAGTGG ATCCCCCTTC 240
 CCCCCTTCCT TCTGTCCCCC TCGAG 265

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAATTCGGCC TTCATGGCCT ACCAAAACAA AAGAAGAAAT CATTTCATC ATGCTTAGAA 60
 AGATGTCAAG AGGATGGAGG ACTCACATTC TGTTAACTCT TCTGCCTGTA ATATATGCTT 120
 TAAACACTAA AAATGATGAG CATGAATCTG CAATTCAAGC CCTCAAAGAT GCTCATGAAG 180
 AAGAAATTCA ACAAAATTCTT GCTGAAACAA GAGAAAAAAT ATTGCAGTAT AAAAGCAAAG 240
 TAACAGAGGA GCTAGACCTT AGAAGAAAGA TTCAAGTTTT AGAATCATCA TTAGAAGATC 300
 ACAATCTCGA G 311

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GCGATTGAAT TCTAGACCTG CCTCGAACTC GTGGCCTCAA GTGATCCACC TGCCTCACCC 60
 TCATCACCTG CCAAGTCCTA CCCATTCTAA CCCTGATAGC TCTTAAATCA GGTCTTTCCA 120
 CCTCAACCTC ATTATCACTG CTCTAGAGCT CAAGCCTTCA GTGTCCTTTC ACTTCTTGAA 180
 TTTACTGTCT TAGTGCTCTT GCTCACATTG TATTCTNTGC CCAAATGCT CTTACCACTC 240
 CCNTTCTTTC TCGAG 255

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAATTCGGCC TTCATGNCCT ACTTGATT ATCACAGTAG CATTGTCTT CAATCTGTGT 60
 GTTAACTAGA AATCAAGGAA AGACATGAGG AGATTGTCT ACTGCAAGGT GGTCTTAGCC 120
 ACTTCGCTGA TGTGGGTTCT TGTGATGTC TTCTTACTGC TGTAATTGTAAC 180
 AAATGTGATG ACAAGAAGGA GAGATCTCTG CTGCCTGCAT TGAGGGAGAT CCGCACGCAG 240
 CTGGTGGAGC AGTTCAAATG TCTGGAGCAG CAATCAGAGT CGCGACTGCA GCTGCTTCAA 300
 GACCTCCAGG AGTTTTTCCG CCGGAAAGCT GAGATTGAGC TCGAG 345

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

GAATTCGGCC TTCATGGCCT AATCCTCCAG ATTATTATGG ATATGAAGAT TATTATGATT      60
ATTATGGTTA TGATTACCAT AACTATCGTG GTGGATATGA AGATCCATAC TATGGTTATG      120
AAGATTTTCA AGTTGGAGCT AGAGGAAGGG GTGGTAGAGG AGCAAGGGGT GCTGCTCCAT      180
CCAGAGGTCG TGGGGCTGCT CCTCCCCGCG GTAGAGCCGG TTATTCACAG AGAGGAGGTC      240
CTGGATCAGC AAGAGGCGTT CGAGGTGCGA GAGGAGGTGC CCAACAACAA TGATCTCGAG      300

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

GAATTCGGCC TTCATGGCCT AAAAAAAGA AGTTTATTTA AAGAACTCT ATAAGAGCAG      60
CTTGGATTTT ATATCTTTAG ATCCAGAGTT TTTACTTTTC TGGAAATTA TATAATTGTT      120
TGGAAATTAC TCTTTATTGT TGAATTTTAA AGCGTGACTA AAGTAGTGCT TCTTAAGATA      180
ATTGTCATGT GTTTTGTGTT TGTGTTGTTT TGTTTTTGG TGCTGAGTGT TGCTCTGTCTG      240
CTCAGACTGG AGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

GAATTCGGCC TTCATGGCCT ACAATTCGGA TAAAGTTTAA GGTCAGCTGA TGAAGAACAC      60
TCAAACCAAA GTCGCCCAT TGGAGAGCGC CCTACCTCAC AGGAATAGGC CTGCATTATT      120
AGTATACCTT CTTCAATCAG TTATTGTTAT TCTTATGGAA ACAACCCATG GGAATGTAG      180
CCTTGGCATG ACTGTATCAA TGGATTGAGA GAGCAGTAGC GGGGACCCCG CAGTCAATT      240
ACGTTCCACA GCAAGTCTCG AG

```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```
GAATTCGGCC TTTCATGGCC TAAATCTCAT AAATAGAAAG NAAAATAATC TAGAAATTTT      60
TCAAAGCTAG TACTCTTTCT CCTTATAAAT GTACACAATT TTAATCTTTT TACAAATTIA      120
TTTAACTGTA CCTACTGTAC TTATTGTAGA TTCAATGACG CAGTTAAGTC ATCACCCAAG      180
GATTTATGAA TTTGAGATTA CTGACCTGTT TTCITCATAT TGCATTACA TCAATATTG      240
TGAATTGTGTT GTTCAGCTTT TCATTCAAAC AAAAAATATT CCCCCAAGAA AACTCGAG      298
```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```
GCGATTGAGT TCTCCCTGCT GGTTCCTTTG AATCACACCA AATGAATGGC TTGCTACTGT      60
TCCCTCACAC CTTTCATATTG TCCATGGTTT TTCCCACCTC CTTAGCTATA CAGCTGCTGT      120
TCCTCCTGCC TAAAATGTCT GAACATTCCC TCAGTGTTC GCTCAGCCCA CATCTTACAT      180
CTTCCCTAAG GATGTTTTTC TGCTGCTATC ATTCATTTTC TTCCTATGAG TTCCTCTGTT      240
ATATTGCGCC ACCAGAACTC GAG                                          263
```

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

```
GAATTGGGCC TTCATGGCCT AGCCCCGACT AGCTTTGCCC TAACTCCTTC ATCAAAAGAC      60
CCCCCGCCAG CTTCCACAC CTATACGCA GCCACATCTG CCCTATTCTC CATGCTTTCC      120
AGCTTGCCCTG CCCTTCCTCA TCTCTCCCTG CCTGTGCAGA CCTCCACCCT TCTTTCTCTC      180
ACCCCTCCAT CCCCCAATGC TTGTAGACCT TCCATTCATT CCGTCTCATC GTGCGTGGTC      240
TCTGATCGTC CATCACCTGA CCTCGAG                                          267
```

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC TTCATGGCCT AGCCAAAATC ACAAGAAAAA TAACTTTGAC TTTGAAAACA	60
AATAAGTTAG AAATGCAGTG TTTGCACTTC GTGGTTTATG TTTGCTTTGG TGGCCTCTCA	120
TTCCCACTTA GCCTCAGTCT CCAGGGCCTG GGCTCCACCA AGGAAGACTC CATCTGCTCT	180
CTCTATTGTC ACACTGGGAA CTTTTTTCCC CAAGGTACAG GATATGATTG AGGGTTTATG	240
GATGACCTCC CACCCCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCGGCT TCATGGCCTA CCTATTCCCA AACTTTAAAT GTTGTCTACC AAATACTGAC	60
AATTATGAAA ATTCTACCAG TAGAACACAC CTCCTTTTG AGCTCCAGAG CACATGCTTG	120
ACATCTCATA TTAGAAAGAA TCTTGATTTC CCCTCCAGTC TAGTCTTTCA TGTTTTGTTT	180
TTCTTTGTGA GAGTCTCCCT CAGCCTGCAA TGGCGTGATC TCGGCTCACT TCAACCTCCC	240
GTGCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTTGTTT NAAAAAAAAA AAAAAAAAAA AGGGCNGGGG GGAAAAAAAA AAAAAAGAAC	60
TCCTGGAGAG GGAAATAGCA AATGTGTCTT GCCTTTTGTG GCTCTCTCTC TCTTTTTTTT	120
TCTCTCGCTC TCTTTCTTTC TCTTCTTCTC TCTGTTTTTA AGTCAAGCAT TGGTCTCGAG	180

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

NNNNNNNNNN NNNNNNNNNN NNNNNNNANN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	60
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	120
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	180
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	240

```

NNNNNNNNNA NNNNNNNNAN NNNNNNANNN NNNNNNANAN GNANNNNNNN NNNNNNNNNN 300
NNANANANNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNC CCCCTTTGTC 360
ATNGTTNTCG TTCCCNNTCT TCCTTGTTTC TTTTTCGGCA CAATATTCA AGNTATACCA 420
AGCATACAAT CAACTCCAAG NTCGGAATTT TAATTACTTC ATGGCCTACT TGATGCAGGC 480
TGAATGTTA TCCCTGGGGT GTGCTTGGAC CCCACCTGCT TTCTTTCTCT CCTGCCCCCTC 540
CCCTACTCTC ACTGTAATTT ATGGACCCTG CCCGCCTGCG TGTGTGTGT ATGTCCTGTG 600
CCTTTTCTCA CTATTGTTTG GGTGTGGGAG GGGGTGTTT TTTACTGAAA AGGGGGGTAC 660
ACCTATAGCT TTCTTGATGT TCAATCAATC AGTCACTGTG TCCCAGACAT ATTCAATAAA 720
CACAGATTGG TACCATCTCG AG 742

```

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

GCGATTGAAT TCTAGACCCG CCCAGGAGC CTCAGCTGC CTAACCAGTG CCATTCTTTC 60
ACAACACGAT TTTCTACAAA TCTACAGCAC AACCGAGTTT GTAACCCGTG GGTTAGTATG 120
AGGACCGGGT TCGTGACTC TCTGTATCTC CTCCTAAGCT TCGTCCAGGG TTCTTTATTT 180
TTGTCTGCTG CCAATGTCGT CTCGCATGCC TGCACCCTCG CATGCACGCT GCCCGCATGC 240
CACGTGCCAC GCTGTAGCCA CATCCTCGAG 270

```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

GAATTCGGCC TTCATGGCCT AGTTGATGTC CTCTCATATT TTGTGTTTA AATACGCAGT 60
GTGGTGGTTG TTATTAGGA CTGCCTCTGC TCTGACAGAT GTGTCTACTC TACAGAGAGA 120
GAGAGAGACT GTGTCTATTG TCCCACCAGG CTGTCCAGAT CCAAACCTCA ATGACCTTTC 180
TGCACCTGTC CTGGCTATTG GTTACAGTTT ACATTCTACC TTCTCCCAAG GTATTGAGGG 240
AGGCTTGCAT GCAATTCTCG AG 262

```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

GAATTCTAGA CCTGCCTCTC CTGACACGGG CCACCAAACC CCTTACCTGG TTCCTTGCTG 60

```

```

TAAAACTTCA CCAAATGAAG CCAGAGTTGA TCATGACCCT CTCGTGCTCG AATCCCTTCT      120
GGGCTCCCTT CTGCCCCCTG CAAAGCCCAC ATGATACCAC AGAGAAGACC TGTCCCTTGC      180
AGGCCAGCTG CTTTCAGCTC TTCCCTCACA CACATCGTCC CGCACACGGC AGCCACCATG      240
GACTCAACAT CCCCAGACACA CGGTGCTGCC CTCTGCATGC ACCGACCCCC TGCCCTCCCC      300
ACCAGCTCGA G                                     311

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

GAATTCGGCC TTCATGGCCT ACCTAGGTGC TTTTAAAAT ATTCAGACAA ATATCTATCT      60
TACATTGATT AAACCCGTGT AAATTCATTT GCAGTATCTA CATCGAATGT CAAAAAAGTA      120
TACTTATTTT TGTTCCATAC TTATGTACAA TTTTTCCTT CTTCAGGCTT TTTCATTTAC      180
CTTTTGAAA AAGCACTTAC TCTCCCTTC CCTATCACCC CATCCCTCG AG                232

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```

GAATTCGGCC TTCATGGCCT ACAGTTGTTC ATACTTCCTT TACAAATATA AAGATAGCTG      60
TTTAGGATAT TTTGTTACAT TTTTGTAAT TTTGAAATG CTAGTAATGT GTTTTCACCA      120
GCAAGTATTT GTTGCAAACT TAATGTCATT TTCCTTAAGA TGGTTACAGC TATGTAACCT      180
GTATTATTCT GGACGGACAC TCGAG                                     205

```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```

GAATTCGGCC TTCATGGCCT AGGGCTTGTC TTTTTCATTG TTGAGTTGCA GGAGTTCTTT      60
ACATATTCTG GATACTAGAC CCTCATCAGA TATGGTTTAA AAATACTTTC TCTCATTCTT      120
TTCACTTTCA AGTATCCCTT TGATGCACAC ACCCAAAAAA GCAAATAGTG TCCAATTGCA      180
TCTTTTGATG AAGAAGAATA CAAGCAGTAA GTCAATTACA GCCTATTTT TTCTTTTCTT      240
TCTTTTCTTT TCTCTCTCTC TCTTTCTTTC TTTGAGGCAG GTAGGCCATG AAGGCCGAA      299

```

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```
GAATTCTAGA CCTGCCTCGA GCTCCAGCTG CCAACACCCT TGGACACAAT ATTCCAGTCT    60
CCACTGCCCA TCTCATGTGG TTCAGGTTCC TCGAG                                95
```

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
GATGCTTGGC TCACTCCCCG CTACTGGCCC CCAGACTTTT CCACCCAGG AAATGTCTCC    60
CCTGCCTGCA GCTTCAGCGA AAGCCCAGGA GGCAGGCCAA TCACTTGAG              109
```

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
GAATTCGGCC TTCATGGCCT ACACATTCTT GTACCTGGAA AAAAAATGTA TCTTATTTTT    60
GATAATGGCT CTTAAATCTT TAAACACACA CACAAAATCG TTCTTTACTT TCATTTTGAT    120
TCTTTTAAAT CTGTCTAGTT GTAAGTCTAA TATGATGCAT TTAAAGATGG AGTCCCTCCC    180
TCCTACTTCC CTCACTCCCT TTCTCCTTG CTTATTTTTC CTACCTTCCC TTCCTCTTGT    240
CTCCCCACTC GAG                                                         253
```

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

GAATTCGGCC TTCATGGCCT AGGTTGTAAG TGA1TTTATT TTTTCTTTTC TATTTTCCAG      60
TGTTTCTGTA ATGCTTTTCAT ATTTCTTTTG GTAGTTAGAA AATAAAGGCT AATTTT1TAAA      120
AAGAAATATCA TAGTCTAAAA AATTAAAGGA TGCATAGAGT TCCTCTTGA CTATGTGACA      180
TCTAAACTGA ATGAACTGTC TGCCTGGCAC AGTGGAACAG CGCAGTCTCA GGATTCTGAC      240
AGATTTT1TGG ATCCCAGCTC TACCACTAAC CTTGGGCAGG ATTTTAGTCC CTCTGAGACC      300
TGCTTTCTCG ATTGAATTCT AGACCTGCCT CGAG                                     334

```

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

GAATTCGGCC TTCACCTAAA TACTCCTCCT TTTGTATCAT TCAGCCTTTT GTTTTAGTTT      60
GGTAAGTTTT AAGAAATTTT AGCAGCAAAG TTGTTATTCA GTGGGCACGA TGGACTCCAA      120
ATGCCTCAAG TTATGTATAC CTGTGGAGGT CACGTACTTC CAAATTGTTC TCTTCCTCAT      180
CTTCTCCCTT TACCTGCACG CCCAGGTGCG CCAGCCGGGC CTCGAG                     226

```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

GAATTAAAAT AAACAAAAGG CAGCCAAGGA TGAAAGGATT TAGTTCTAAG ATGTTTCACA      60
GTTGTGATTT GTTTATTTTA ATCCTTAGTA GTAAATTAGT ACTAGAAGGA TCAGGTATAT      120
CTTCCTTAAT TCTTCCAGG GGAGAGAAAG TCCCATTTCT CGAG                     164

```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

GAATTCGGCC TTCATGGCCT AAGCCTATGT TGATCTTGAA CTCCTGGGCT CAANCCNTCC      60
TCCTGTCTCG GCCTCCCAA TTGCTGGAAT TATAAGCACA TTACACAGTG CCCAGTCTAC      120
CTACATTTTG ACAGACATAT AATATTCCAT GGCATGGTTA CATTATTGAG TTAAGAATGT      180
TCCCGGTTTT CTCTAAGATA ATGCTGCCCA TCTGTGCTC ACTCTGGACA TGTAGAGTAC      240
CTGCAAAGAC TTGGACTGCT TGAGCAGAGG GCCTGCTTTT GTTTTTTGTT CTCCTGCCT      300
GTTGTAAC1TT GATGCTGCCA AATGATCCTC TTA1AATGATT GTACCACCTT CCCTGCCACC      360
ACCAGATTTT AAGGATTCTC TGTACCTCCC AACACATGAT GACATCATAC ATGAAAAGTT      420

```

TTGCCTGCCT GATGGAATAA TTGAGTCAAG AAATAGGATG CTAATGGCAT CTTCGCTTAC 480
CCGGTCTCCT CGAG 494

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GAATTCGGCC TTCATGGCCT AGTTGGGTGT TGAGCTTGAA CGCTTTCCTTA ATTGGTGGCT 60
GCTTTTAGGC CTAATATGGG TGTTAAATTT TTTACTCTCT CTACAAGGTT TTTTCCTAGT 120
GTCCAAAGAG CTGTTCTCTT TTGGACTAAC AGTTGTCCTG ATGAATAATT TCATTTTCCT 180
CAAGTTTATG ACACTCGGAA CGTCAAGAAC TGGAGGTTTG TGCAATTTGA GACCGGTCGG 240
CACTGTGCAG AGATCAGAGT ACTAAGAGAC AGAGATTAAA ATGGCTATCC TCGAG 295

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GAATTCGGCC TTCATGGCCT ACAAGGATAG AATTCATTCC ACCTATATGT ACTTAGCAGG 60
GAGTATTGGT TTAACAGCTT TGCTGCCAT AGCAATCAGC AGAACGCCTG TTCTCATGAA 120
CTTCATGATG AGAGGCTCTT GGGTGACAAT TGGTGTGACC TTTGCAGCCA TGGTTGGAGC 180
TGGAATGCTG GTACGATCAA TACCATATGA CCAGAGCCCA GGCCCAAAGC ATCTTGCTTG 240
GTTGCTACAT TCTGGTGTGA TGGGTGCAGT GGTGGCTCCT CTGACAATAT TAGGGGGTCC 300
TCTTCTCATC AGAGCTGCAT GGTACACAGC TGGCATTGTG GGAGGCCTCT CCACTGTGGC 360
CATGTGTGCG CCCAGTGAAA AGTTTCTGAA CATGGGTGCA CCCAGGGAG TGCTCGAG 418

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC TTCATGGCCT ACAGACATCT AATCGGAATC TTGCTCTGTG TGCCAGGCT 60
GGAGTGTAAT GGCACAATCT CGGCTTACTG CAACCTCTGC CTCCTGGATT CAAGTGATTC 120
TCCTGCCTCA GCCTCCCAAG TANCTGGGAT TACAGCCCTG AAAACCACTC GCTTGCAAG 180
CGCTGGATCA GCAATGCCTA CTAGTTCTTC ATTCAAACAC CGGATTAAAG AGCAGGAAGA 240
CTACATCCGA GATTGGACTG CTCATCGAGA AGAGATAGCC AGGATCAGCC AAGATCTTGC 300
TCTCATTGCT CGGGAGATCA ACGATGTAGC AGGAGAGATA GATTCAGTGA CTTCATCAGG 360

```

CACTGCCCCCT AGTACCACAG TAAGCACTGC TGCCACCACC CCTGGCTCTG CCATAGACAC      420
TAGAGAAGAG TTGGTTGATC GTGTTTTTGA TGAAAGCTCA ACTTCCAAAA GATTCTCTCA      480
TTAGTTCATT CAAAAACACC AGAAGGAAAC AACGGTCGAT CTGGTGATCC AAGACCTCAA      540
GCAGCAGAGC CTCCCGATCA CTTAACAATT ACAATGCGGG AACTCGAG      588

```

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

GAATTCGGCC TTCATGGCCT ACGACTGGGG GAAATGTCTA TTCTCCTGTG TATCTCTGGG      60
CTTTTCTTGT TTTTGGCTGC CTCCTGCTCA GTTCTCTCTT TTAGGTATTT AGTAAAGCGT      120
TCATGTAATG TCATTCTCTGA GGACCCAAAG TGATGCTCTT TAACATGGTG AACAAATGGTC      180
ACTATATGTT GGGCAAACAG TTCTGAGGGG CTACGCTGAG ACTGAGCTGA TTGTATGTGC      240
TGGAAAATGG AACGAACTC CTGTCCTTT TTGTGCTAT GGACTAGATC TCGGCAAAGC      300
TTGCGTTCCT GAGCCAATAA GCCACTGGGT CGTGCGAGGT CCTCATCAA AGAGTCCATC      360
CGGACATTGA CCTGTGCCTC TCGAG      385

```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

GAATTCGGCC TTCATGGCCT AGCAGTTCAC CACTGCAAAA CCACGGGGCT GCGTGGAGGT      60
ATTCATGGGA CACCGAGTGG TATCACTAGC AGCGGACTCT GCATGCTTAC TTAGAGCATA      120
AAAGGATAGC ACCCTTGGCC ATTGCCTGAC ATGAACTCAG TTTGGAAATT GCAGAGGTGT      180
GGAGAGCCAT GGATGGGTTT TATAATTAT TCTAATGTAA TCTCTGTGCT AAAGGCTGTT      240
TGAAAAAAT AATGAAGTTG ATGTTGCTTA AGTTATATGC AAATGTAAAC TGGTCTTCCT      300
TCAAGATGTT TGGAATGGAA TGAATGCCCT TCCCCTGGGT ACCTCCCAAT ACCTACCCTC      360
AAAAGAGCTC CAGTAAGGCT TCCTTATCTT TCCTTGCCCT GCTTCCTACA CTGCTGCTGC      420
AGGTGTCTCT GGGTGATTGT GGGGGAAACC ACTGTGGTTA AGCACCAACA CCAAGACTCG      480
AG

```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

GAATTCGGCC TTCATGGCCT AAGGCCTTGC TGCCTGTGG GTGGACTCTG GGGAGGCCAG      60
GGGCCCCAAGG CCACCTTCTA GGGCCTGAGG AGCCCTCTGA GACCTGCACA CCCACCCAG      120
GGAGCGCCCC TCCCTCCACC TCTGTGCCCC CCCAGTGA CTGGAACCTC TGTCTGTTTT      180
GCAGATTCAT CCGGAAGGGC CGCCAGCCAG TGGATTCCC GGGCCCTCAG CCCTCTGGAG      240
TGTACGAGTT TTGGAGAAAC CTCTTCCTCT GTATATGCTT TTGACTTTCC TGGACTGATG      300
TAAAAATACT CTTTTCTTTG ACCTGTTTAT TTTTAAGACA CGACGTGATT GTGTCAGCTT      360
ATATTTTATT GCTGAAGTAA ATTTTCAAAT GTTTTATTAG TTTTGTGGA TCTTTGTCTG      420
CTCATTTTGG AGTTTTTCTA ATTTTGATAG GTGTTCTTTT ATGCTTTGTA TTGTTTCTT      480
AATGACTTTT ACCTTAGTTT TTAACAAACC CATAGTACAG TGTACCCTCG AG              532

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

GAATTCGGCC TTCATGGCCT ACATTTTGG AAAAAAAAAA ATCTACTTTG TGTATGTGTG      60
GGGTGTGGGG TGTGAGAGAT ACATTCCTTT TNGTGTCTA AATCTCACAG TCCACATATG      120
ACTTTCCCA CTTGAGAATT CTCTCTCATC TGTGTGGCTC CCTGCATTCT ATAAAAATAT      180
AAATAAATAA AATTTTAAAA AGTATAAAGC CGGTGCCATG AGACCCTTGG GTTGGGCAAA      240
GCCTGTGAAG TTTGAACCGG TTAACGCACG AATACAAGGG AGTGATTATT ACAAGGCCAT      300
CCCGCTTAGC ATCGGGGAAT CATTTGGGGA GAGAGATTCA ATTTCAATAA GATGATTTTC      360
AAGGGCTGTC TCGAG

```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

GAATTCGGCC TTCATGGCCT ACACGCGGTC AACTCTGCAG GGCTGATGAT AAACATGCCT      60
CTTCTCCTAT TGTCTTCTC CTCTCTAAAG CAAGGTCATT TCTGTGCTCG TCAGGCAGTG      120
GCAGGGGTG GGAGGAGGAG AGAGGGAAAC ACTGTGGTCA GGCTCTGGGG AGAGTTGACT      180
ACAGTGTAGC TCTTGGATTA TTTATGAATA TTGCCCTCAG ATTTATTTTC ACTCTGCTCC      240
TTCCATT CAT ATTCCAGAG ACAACCAAGA GCCGACTGTA GAAAAAGACT TCCAGACACC      300
TAGAATATAT ATCAATAGAC ACTGTTTAAA AGGGGAGACT CGAG

```

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

```

TGGCCTAAAG GGGGTGGGTA CTCCGGTGGG GTAAGGTCAG AAGGTCCTG TGCAGGGAGG      60
GACTGGTCCC TTGAGAAGGA ACAGAGGGCA AATCCTGAAG AGTCCTGGAG GCCCAATGTA      120
GACAGCAGAA GCTGGGAGCT GACCTAGGAG TGATCGGGGG CCTGATCCAG ACAGGACAGA      180
CACAGGCTGA CACCGGAGAG TCCCAGGTGC CAACATGAAC AGTTAAGGCA GGGGCTGACC      240
CCAAAGAAAT CAGGGGCCCCG CAGCTGACCC CGGAGGGTCC CAGGTGCCGA CCTAGACAGC      300
AAAGGCAGGG CTGACCCCGAG AGGGTCCCGA GCCGACCCAG ACGACACAGG CAGGGCTGAT      360
CCCGGAGGGC CCCGCCCCGA CCCGGACAGG CAGTGAAGGC ACAGGCAGGG CTGACACTCG      420
AG

```

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```

GGGAACGAAA GATGGCGGCG GAAACGCTGC TGTCCAGTTT GTTAGGACTG CTGCTTCTGG      60
GACTCCTGTT ACCCGCAAGT CTGACCGGCG GTGTCGGGAG CCTGAACCTG GAGGAGCTGA      120
GTGAGATGCG TTATGGGATC GAGATCCTGC CGTTGCCTGT CATGGGAGGG CAGAGCCAAT      180
CTTCGGACGT GGTGATTGTC TCCTCTAAGT ACAAACAGCG CTATGAGTGT CGCCTGCCAG      240
CTGGAGCTAT TCACTTCAG CGTGAAAGGG AGGAGGAAAC ACCTGCTTAC CAAGGGCCTG      300
GGATCCCTGA GTTGTGAGC CACCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```

GAATTCGGCC TTCATGGCCT AAAACAGATA ACGCTATAGA GAAAACACTG TTTACTGAAC      60
AGTGCTTTGA AACCACGAGG GTGATCAGAG CCCCATTTTCG CCTTCTAGAG ATAAACCTGT      120
CTCCCTTCCT GCAGAGCTAG CTCTCCTAT TGCTTCTGGT TGTGTTTGT CTTCACTCTG      180
CTTCCTGCCA GTGCAGCAGC TCCTGCTAGA TCTTGACATC CTAGTGGCCA GATCCCAGGG      240
GCGGTGCTGG TCCTATCCGA GCTCTCTGCC TCATCTCCCA TTCCTTTTTT CCACACTCAG      300
TGTGTATTCT CTTGGATTTC CATACCCTGT TCCTCCTACC ATCCACCTCT CTACCTCATC      360
TCCCGACCTG CCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```

GAATTCGGCC TTCATGGCCT AGCAGGTCAG GAGCCCGGG AAGGCCCAGA GGTACTCCAA      60
AGGGGGCCGG CTGGTATCTG AAGGCCCTT GCAGTTAGTG TGTGTGTGAG CTGTGGGCAT      120
GAACATGCCA CAGGCAGACA CTGTTTAGCC AGGGTTTAA GAAACACGGA GGGTCCTGTG      180
GATCTGGAGT TCATTTGTCA GGACAGGGAT GGGGACCCCT CTGAAGTAT CACTGTGGGC      240
TGAGGGGTGC TGGCCACACA ACCTCTGTGG GAGGCATCTC TTGCAGTGAA GCTGTGTGGTC      300
CTCAGTTCAG TGCCCACTGA GGGTAACCAG GCCCCAGCTC TGCACCCCA CTCGAG      356

```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

GAATTCTAGA CCTGCCGCGAG CACAATCCCG TGGACAGAGC TTAATCCATC TAACTCGTTT      60
TCAAGTGCAAT GATTTCACCT TTCACTTTC CTTTTCCTT ATTATGTTGC TTAACCTGTA      120
CAGTGGCAAC TGAATGCAAT TTCAGAAATA GGAGGTTTCG TCCAGCACCC TCTGCAGCCT      180
TGGTGCTGT AGCTCTGGAC TTCCCTGGGC CTTTCCCTGT GGGAGGGCCC TGTAGACCAC      240
ATCAGGGTGG GGTGGGGGTC ACTTGGCAAA AAGGGCCGAG GTCTGGTGAT GTGGTTCCTCA      300
GGATCTGGAA CCTCTCCAC CCCTCCTGCA GTTGGACTGA ATTCTTCCTT TTCATCCGAA      360
GAAACCCACT TGCTGTTTCC AGCCAACTCG AG      392

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

GCAAGATGGC GACCGAGACG GTGGAGCTCC ATAAGCTAAA GCTTGCCGAA CTAAAGCAAG      60
AATGTCTTGC TCGTGGTTTG GAGACCAAGG GAATAAGCA AGATCTTATC CACAGACTCC      120
AGGCATATCT TGAAGAACAT GCTGAAGAGG AGGCAAATGA AGAAGATGTA CTGGGAGATG      180
AAACAGAGGA AGAAGAAACA AAGCCCATG AGCTCCCTGT CAAAGAGGAA GAACCCCTG      240
AAAAAACTGT TGATGTGGCT CTCGAG      266

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

GAATTCGGCC TTCATGGCCT AAACAATGAA TAAAGCCAAG CCAGTTCCTG CCCCCGTGGA      60

```

GCTTGTAGTC	AAGACATTGA	ACAAGTGATC	AGAAAGATGT	TGACTGCTGC	AGCAGAGGGT	120
TGCAAGCTGC	TCATGAGTAT	ATAACAAGTA	CCCCTAACCA	AAGCATTCTC	TCCCTTGGTT	180
TAATGTCCAC	CCATTGAGGT	GACTGCTAAA	TACTAATCCA	TGACTCTATC	CCTTGGCATT	240
CAAACTCACA	CATCCACTTA	CCTGCCTCTC	CAACCTCCCT	GCCTCGAG		288

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GAATTCGGCC	TTCATGGCCT	AGTCTCTGCC	ATGTTCTAAA	CTGAAAACCT	CCTAGTCAAC	60
TTCACACTTT	ATTCCCTGAT	CCTCAATTGG	TTCCCATGTC	CCGTTAGTGT	TTCTTGTAAG	120
CCTCTGCCAC	CACCGCAGAT	CGAACTCTAA	TCACATCTCA	CCTGAATTAT	GGAAAAGTCA	180
CCTCAATTCT	CTCACCCATC	CCAGCCTCCA	CTATGGATTA	ATATGCCTAA	AGCAGAGCTG	240
ACCACAACGG	TGAGAAGAAT	CTGAGAGGGA	AGCAGCAGCA	AACACAAGAG	TCCTGGACA	300
TGCATGCCTC	GAG					313

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCGGCC	TTCATGGCCT	AAGAAAAAAG	GATAGACAAA	TAGTATTTTT	GTGATTTTAC	60
AGTAGCTTAA	AACTATAGGA	TTTTTTTCC	CCATTACTTT	GCAACAACCTG	ATACTTTTGA	120
CCAGTTCTCT	TTCTTAAGCA	TTTCTCTCCT	TGAGCTATTA	CCCAAATTGT	CCTAGTTCTT	180
CTCTGCTTGT	CCCTCAGCTA	TACACAGTCA	CTGAGGCTCT	GTGCTTGGCT	TCTGTTCCCT	240
TCTCCTCATA	GGGATTCCTC	ATGTTGGAGT	TCATCAAGCT	CGAG		284

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC	TTCATGGCCT	ACCACGATAG	ACCAGCTGTA	GCTCATTCCA	GCCTGTACCT	60
TGGATGAGGG	GTAGCCTCCC	ACTGCATCCC	ATCCTGAATA	TCCTTTGCAA	CTCCCCAAGA	120
GTGCTTATTT	AAGTGTTAAT	ACTTTTAAGA	GAAGTGGGAC	GATTAATTGT	GGATCTCCCC	180
CTGCCCATTG	CCTGCTTGAG	GGGCACCACT	ACTCCAGCCC	AGAAGGAAAG	GGGGGCAGCT	240
CAGTGGCCCC	AAGAGGGAGC	TGATATCATG	AGGATAACAT	TGGCGGGAGG	GGAGTTAACT	300

GGCAGGGCAC TCGAG

315

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GAATTCGGCC TTCATGGCCT AAAGATGTTA GATATTACAA TTTGACTGAA GAACAGAAGG	60
CGATCAAGGC CAAGTATCCG CCAGTCAATA GGAAGTACGA GTGTGAGAGA TGACTTACAG	120
TCTCTTCTGT TTTCACTTTT GGATGAATGG CTTTATAAGT TCAGTGCTGA TGAATCTTC	180
ATACCCCGGG TGGGAGAAG AATTTTCATT GTCCAAGCAC CCTCAGGGA CAGAAGTCAA	240
AGCAATAACA TATTCAGCAA TGCAGTCTA TAATGAAGAG AACCCG	286

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GAATTCGGCC TTCATGGCCT ACCTCTGTGA AAATTTAATT TTTTATATCC TGATTAATAT	60
ATTGTGACTT TAGGCCCAT TTTTCATGTG TTTCACTTGA TAGAGTTAAT CCATAAAATT	120
GCTCTTTACT TTAGCTTATC AAATGAAGTA TTATTTTGTG GACTGGAGGC CAAAAAGTCA	180
ATGTGAGCTT CTCACAGGTT TTAAAGCTC CACTAAAAAT AATTATCCAC TTGTCTTTAC	240
TTTTGTTGAC CAGAATAGTT GGTAACCTG CCAGAGCCTG TACTTACCTG CCAAAAACAA	300
TTAAATCTGG TTAATGCCTG AAACCAAATC TCTCAGTCTC AAGTGTATA CTATCCAAGT	360
TTTAAATGGA AAGGTAACT GTGGAGTAAT GAAATTTTGG TTTTACTGTA CCTTTTGCTA	420
TCAAGATAAT ATTCATGTT GAAATCTTGT CTTTATTGG AATTTAGTTA CTGCTGCTT	480
TTAACCTTTG CTTTCCTAAA GAAAGTTTGA GATCCAGAGA GTTCAAGGA TCGGGGAGTC	540
TCGAG	545

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GAATTCGGCC TTCATGGCCT ACAATAAGTG TGTATACTT GCTTTGGTGA TTGCAATCAG	60
CATGGGATTT GGCCATTTCT ATGGACAAT TCAGATTCAG AAGCGTCAAC AGTTAGTCAG	120
AAAGATACAT GAAGATGAAT TGAATGATAT GAAGCATTAT CTTTCCCAGT GTCAACAGGA	180
ACAAGAATCT TTTATAGATT ATAAGTCATT GAAAGAAAAT CTTGCAAGGT GTTGGACACT	240

TACTGAAGCA GAGAAGATGT CCTTTGAAAC TCAGAAAACG AACCTTGCTA CAGAACTCGA 300
G 301

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCGGCC TTCATGGCCT ACACATTTTG ACAGCTTCCT TTCAGGTTTC TTGAGCTCTC 60
AGAAAAATTA GAAGGAAGTG GGCTGGGGAT ATAGAGAGAG TCCAAACTAC CAACTAATGA 120
ATGAATCTGA AGGAGACACA GAAGGGCAAG TAGAGTTTAG AGTTTGAGAG TGCAGGAAAG 180
TTTTGAAATG GTCAGAACTG CCAGAGTAAT TTCTGAGATC TTAATAAGCA CTCTCCCACC 240
GTTTGCCCTTA AAGATACCCC TTCCCCCAA TTGAACATC ACAAATCTGC AGAGCTCTTT 300
AATCAGGTGT GTTATACACA ATGAATTTAA TTCTCTTATT GCCCTGGAAG AAAGATAAAC 360
CAGATGTGGC CCTTGCCCTT TTTCAGTAAG TATTGTAG ATCTTCATTA CATTTTAGGC 420
CTCCTAGGCC ATGAAGGCCG GCCTTCA 447

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GAATTCGGCC TTCATGGCCT AAAATTCGGC TGATTTCCTT CTTGGCTAGC CCAGCTGACG 60
GAGTCAAGAG CAAACCAAGA AAAACTACAG AAGTGACAGG AACAGGTCTT GGAAGGAACA 120
GAAAGAACT GTCTTCCTAT CCAAGCAAA TTTTACGCAG AAAAATGCTG TAATTTCTTG 180
GGAAGATTTT AATGTACACC TATTGTAAA STCATCAGAA TAGTGTGGAT TATTAAATAT 240
CTAGTTTGGA AGAAAATAAT TTATATAAAT TATTGTAAAT TTTTATGTAA ACTCGAG 297

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAATTCGGCC TTCATGGCCT AGAATAAAAC AAAGCCTTTT CTGCCTTTTA CATTCACTTC 60
AGTAACCGTC AACACCCAC CCATATACTC CCATACCATG AGGTGTAATT TTCAACTCC 120
TCGCATACTT TTAATTACTA GTTTAATTAT TTGCCCTCTC ACTGAGTCTA TAATCTCACT 180
TAGGGTAAGA ACAGAACTCA ATTACAGATG CTCAGTAAAC ACTGGAAGGC CGCGGCTCGA 240
G 241

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

GAATTCGGCC TTCATGGCCT AGGGCTGCCC AAGATTGTGA AAGGTAAGTA GTATCTTTAT    60
TTGGGGGTAA CTTAATTATA GATAAAAGAT GGTCCAATAC TGGAAACTGT TCGTTTCTTC    120
CCTTGGATCT AGTCTTCTTC TGCTTTATAT AGAATCCAC CATCATCTCG AG              172

```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

GAATTCGGCC TTCATGGCCT ACACGTGACA GCCTTTCCTT TTTCTAGATCA CCTTCCTCAC    60
ACTGATGGTC TCATACAACA TCATTTTGAA TGTCTCAGC TCTCTGCACC ACCCACCCAA    120
CTCCACTCTG GGCCACCGCT GGTGTATCCA AGATCAGGAC ACCAGTCCCT GGGCACCAGG    180
GAGTATGCTG GCCACTGAAG CAGCTTCGTT TTTCCGGCAC CCATGTTGTA AAATCGACTC    240
CCCCAACTC GAG              253

```

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

GAATTCGGCC TTCATGGCCT AGAAAGTTTA AAGATTAGCG TACTGATTAT GATGGGATTT    60
TTACTGAAAA TTAGTTTTGT CAGGCTGCTT GCTTGTCTGT GTATTTTCTA TTCTAATTTA    120
GTTTTTATTT TTATCAAAGC TGTATTACT TATAATGTAA AAAGTCAATT AGTTTCCAA    180
GGCTTATTAT GGAAACAGT AGTTCCCCAG GCTCCCATCC CTATGTCCAA CAAACTCGAG    240

```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAAGCCTTT GATTATTCAG CTGCCACTGC	60
CTACAGGCCT TCTCCCATAT TCCTTCCTTC TTGCTAAGTC TGACTTAAAC TAGGCTTAGG	120
CACCAACTCC TATAGGAAGC CTTCTTGAA CCTGGCCCTC TACTTTTCAC TCACTGACTA	180
CCACTCAATT AACTGAACGG TGAAAAGTAA CCCACAGCTA CGCATTTCATG CAGACAACAG	240
AATTTTACTA CTTCTTCTCA CTACTGGTTC ATATTTCTGC AACCAGAAAA TATCATTTC	300
TCCCTAGTAA CTATGGCTTC CATCTGTAC TTCC	334

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

GAATTCGGCC TTCATGGCCT AATAATGACT TGTGGTTGA TTGTAGATAT TGGGCTGTTA	60
ATTGTCAAGT CAGTAGGCCA TGAAGGCCGA AG	92

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GAATTCAGTT CCTTATATAT TCTAGTTATT AATCCCTTAT CAGGTGGATA GTTGCAGAT	60
ATCTTCTCCC ATTCTTTAGG TTGTCTCTTC ACTCTGTTGA TCGTTTCCTT TGCTCTGCAA	120
AAGCTTTGTA GCTTGAGATA ATCCATTG TCTGTTTTG CTTTGTGTC CTATGCTTTT	180
GAGGTCTTAC TCAAAAATT TTTGCCAGA CCAGTACCCT TGAAGCATTG CCCCAATGGT	240
TTTTTTTTT AGTCATTCA TAGTTCAGGT CTTACTCGAG	280

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCGGCC TCCATGGCCT ACATAGATGG GCACACTCAC ACACAGAAGT GTGCTGTAC	60
AATCACCACA CACGCACAAA CACACACACA CACTAAAAAT ATAAACACA TGCCTCAT	120

```

GGGCATTTCA GATGATCAGC TCTGTATCTG GTTAAGTCCG TTGCTGGGAT GCACCCTGCA      180
CTAGAGCTGA AAGGAAATTG GACCTCCATG CAGCCCTGAC AGGTTGTGGG CCCGGGCCCT      240
CCCTTTGTGC TTTGTATCTG CAGCTCTTGC GCCTTTTATA AGTCCATCCT AGTCCCTGCT      300
GGATGGCAGG GGGCTGGATG GGGGGCAGGA CTAATACTGA GTGATTGCAG AGTGCTTTAT      360
GAATTCACCT TATTTTATCG AAACCCATTG GACTCGAG      398

```

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```

GTGTCAGAGC AGGCATTTC CAACCTAAGG AAATCTTTGT TTTCAAATAT TAGGGTTTTT      60
TTTAAATTGT GGTAAAGGA TTTTGGACAT GCTTTGTAAA TTGTTAGTAA AAGGACCTAT      120
TTTCCACCTG TATTCTAAGT TATTTTTCCT CCTCTTTTG AATTTTTCAG GTCAGCCCTT      180
CATAAACCCA GATGGGAGTC CAGTTGTGTA TAATCCTCCT ATGACTCAAC AACCAGTTAG      240
ATCCCAAGTG CCTGGACCTC CACAGCCACC TCTGCCAGCC CCACCTCAAC AACCAGCAGC      300
TAATCACATT TTCTCACAGG CGCATCTCGA G      331

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

GCTGCCTCGA GGTCTCCAAG ACTTTTTCAT CTCGTATCGT TTCGGGATCC GTATCCATAC      60
TTTTATTTTC ACTTCTTCC TCTTCTCCT CGAACTCCTC GTCGCCATCC TGTCTGCCCA      120
GCTTCCCGTA GCCATCCTCG CCTTCTTCT CGTGCTCCTT CTCGCTCTCG CCATCCCTCG      180
GCATACTCTC CCTTCTCTC TCGAG      205

```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```

CAAAAGAGAT GGTACCAGCA AGAGATTAAT ACTAAAGAAA TGCAGTCAGA TTTAAAGAA      60
ACTGGAAGAA GAGCCATTTC TCCAGGGGAG AAGATTCTAG ATGTGATTGA TGACACCATA      120
GAAATGGAGA CAGGTCTGAA AGCAATGGGA AGAGAGATT GTCTAAGGGA GAAGACGCCA      180
GAGGTGATTG ATGCCACTGA GGAAATAGAC AAAGATTGG AAGAAGCTGG AAGAAGAGAA      240
ATATCCCCAC AGAAAAATGG CCCAGAGGAG GTTAAGCCTC TAGGTGAAGT GGAGACAGAT      300

```

TTGAAAGCAA	CTGGATATGA	GAGTTCCCCA	AGGGAGAAGA	CACCAGAGGT	GACTGATGCC	360
ACTGAGGAAA	TAGACAAAAA	TTTGAAGAA	ACTGGAAGAA	GAAAAATATC	CCCAAGGGAA	420
AATGGCCCAG	AGGAGGTCAA	GCCTGTAGAT	GAAATGGAGA	CAGATTTGAA	CGCAACTGGA	480
AGAGAGAGTT	CTCCAAGGGA	GAAGACACCA	GAGGTGATTG	ATGCTACTGA	GGAAATAGAT	540
TTGGAAGAAA	CTGAAAGAGA	AGTATCCCCA	CAGGAAAAC	CGAG		584

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GAATTCGGCC	TTCATGGCCT	ATGCTTCTG	AATTGGCAAG	ATATTCAGG	CTTATTTGGC	60
ATTTCATCTTA	CTCTAGACCT	ATTATCAACC	ATGTCTCCAA	GGATAAGTAG	ATCCTTTTAA	120
GGGAAAATGG	TATTTTGAAA	GCATAGTGTG	GGATCTGAGG	ATACCTATTC	CTGTCAGGTT	180
GCTTATGTT	TGTTTTCAGT	GAGTAGATCT	TGGACTTTAT	TAATTTTATT	TATTATTTT	240
AAGAAAAGTA	CATCATGAGT	TATAAGTAAT	AATTCCAAC	CAAATTTTAA	TATTGCTTAA	300
CTTCTTTGAT	TTTATATTTA	TCTTTTACAC	TGAAAAGTCT	CGAG		344

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GCGGGTGGAC	AAAAATGAAG	CCAATGAAGA	AGGCATGCAC	TGGCCTTTCA	GGTCCTGGCA	60
GTGGCAGCAA	GTCCCCCCCC	GCCACCAGGG	CCAAGGCTCT	GAGGCGGCGA	GGGGCTGGGG	120
AGGGTGACAA	GCCAGAGGAG	GAGGATGACG	AGGCACAGCA	GCCGCAACCA	CAGTCCGGGC	180
CCGAAGAGGC	TGAGGAAGGG	GAGGAGGAGG	AGGCTGAGCG	GGGCCCTGGG	GCTGAAGGTC	240
CTCCACTGGA	GCTGCACCCT	GGCGACCCGG	CTCCAGGCCC	AGCAGAGGAC	CCCAAAGGGG	300
ATGGGGAGGC	AGGCCGCTGG	GAGCCCTCAC	TCAGCCGCAA	GACAGCCCCG	TTCAGTCTCG	360
AG						362

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GCACCACCTC	TTGCACTGTG	AGGAGTTTAT	TGATGAATTC	AATGGGCTGC	ACATGTCCAA	60
GGACAAGAGG	ATCAAGTCAG	GGAAGCAGTC	CAGTACCTCC	AAGCTGCTGC	GTGACAGTCG	120

```

AGGCCCGTCG GTTGAGAAAC TGTCCACAG ACCTTCAGAT CCTGGAAAGA GCAAGGGGAC      180
CTCCCATAAA CGGAAGCGAA TTAACCTCC CCTGGCCAAG CCAAAAAAG GGTATTCAGG      240
CAAGCCCTCT TCAGGAGGTG ACAGGGCCAC CAAGACGGTG TCTTACAGGA CTACCCCCAG      300
TGGTTTGCAA ATAATGCCCC TGAAAAAGTC TCAGAACGGG ATGGAATG GGGACGCCGG      360
CTCTGTAAGG ACCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

GATTGTATTG AAAGTCAGAC ATAGGTGTGG AACCAATTAT GGGAGTGAGG ATAAGTCTAG      60
ATTTGGGAAT CAGTCGCAGA GAGGTGGACG ATGAAAGTCT GAGAAGAAAG CATCTTGCTA      120
ATGGAGTGAA CTCAGAGCTT GATAAAGGGA GGATGAGTGG AAATGGAGCT CAACGCTGTG      180
CCTTGGGAAA TACCTCTGTG GATTGGTGGG AGCACAGTGA GAAATTCAAG AAAGACACAG      240
ACAATGGAAT AACCAAGAGAA CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

GAATTCTAGA CCTGCCTCGA GCATTGCCCC CGGCCTAAGA AGCTCTCTTA TCTTGCATCT      60
TGGGCTGGAC TCCTACAACA GCCACAACCT CCGTGCTGGT CTCCCAGCTT CTAGCCTTCC      120
CCCATCTCCT GTCGTTTTCG ACACAGCAGC CAGAAGGATC CTTTAAAAAC AGAGGTTGAT      180
CCTGTCGTTT CTCAAAATCC TCCAATGCTT TTCCTACTGC ACTCAGAGTA AAAGCCAGTC      240
TCTGCCTTAG ATGCTCTGGG ATCCTGTACC CTCTTTGGTC TCATGTCCTA CAATCTGCAT      300
TCTGGCCATA ATGGTCTTCT CTGCTGTTC TGAACATTC CAGGAACATT CCCCCCATAC      360
CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

GAATTCGGCC TTCATGGCCT ACTGGGTTCT GAGAAGCAGT GGCCCGAGCT GAAGCATCCA      60
GACAATGAGT GTTCAGAAGC TGCCAGATTC TCACCTAGCC TTAGAAGTAA CACAGCCACA      120
TTCTGTGGT TACAAACACA TTTCTAAGGC CAGTCCAGAT TCAAACGGAG GGCAATTAGA      180

```

```

TTTGACCCCT TGATGAAGGA GGGCAAGGTT ACACTGAAAA ACAGCATAGG GACTGGGAGA      240
TATTATGATG TCCATTTTGG GAAAATCTGC CACAGACACA GTGAAGACAG AGAGCCCTTC      300
TCTCTGATCG AGGACCTCCA GAATGATCTG CTGAGTCACT CAGGTATGCT GGACCATTCA      360
CACTCACCCC GGAAAAGCTC GAG                                              383

```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

GAGGTTTACA GGTTTAAGCA TTTGTTTTTA CAAAAAGGAA TGGGATATGG GGGTGGTCAA      60
GTTTTACGGG TAATAACAAC ATTCTCTCTA GATGGCAGGG GGTAAGTCTG CCTGTCCTCC      120
ATTGCTGGTA CCACATAAGG GATACATTAG TAAAGTAGGG AAAGGGTCAT ATGTGTGGTT      180
GACCTGTTCT TCAGAGAGGA ACGTGGGATG GTATCTGCTG TGTACCTGTC TCAGACCAAA      240
CCTGGGGGTG GACCAGTGCC CCTTCTTCT CAGCCTTCTT CCACAGCCTG ACTGTACTGC      300
CACCCGCACC CATGAGAAGG AGGTNNTGAA GGAAGCTTGA GGACATCCAC CTCGAG      356

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

GAATTCGGCC TTCATGGCCT ACAACCATTG AAAAAATATA GACTTAGAAA ACGAAAGTTC      60
CCCTTAATCA CAAAGAACCA CAGTTGACAG GGTGATAGA TGTTTTTTCA GATTTTTTTT      120
TTCATATGTC TGCTATCTTT CCCCACAGGA ACTGGGTTTT ATTTTAGGTG TTGTTTTGCA      180
ACCTCTGTTT TTCAGTTGCC AGTTTATCTC AGACATTGTC CTATGTCAGT ACAGGCCCAT      240
CTCGAG                                              246

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

GAATTCGGCC TTCATGGCCT ACAAAAAAAC AACTTTCCAG TGGCTTCTCA CTGCTCTGAG      60
AATAAACTCC AGGCTCTTCC ATTGCAACCA ACAGGATCTG GTGATTCGAC CCCAGCCCCT      120
CTTTCCAGGC CCTCATCACC TGATCCTCC CTTAACCTAT CCTGCTCCAG CTGCACTGGC      180
TGCCTTCCTA TTCCTCCAGC ATACCAAGAT TGTTCCTGCC ACAGGGCCGC CACTCGAG      238

```

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```

GAATTCGGCC TTCATGGCCT AGTTTTTCT ACTCCTACAA GTGTAAATTG AAAAATCTTT      60
ATATTAAAAA AGTAACTGT TATGAAGCTG CTATGTACTA ATAATACTTT GCTTGCCAAA      120
GTGTTTGGGT TTTGTGTGTG TTTGTTGTT TGTGTGTTT TGGTTCATGA ACAACAGTGT      180
CTAGAAACCC ATTTTGAAAG TGGAAATTA TTAAGTCACC TATCACTCGA G                231

```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```

GAATTCGGCC TTCATGGCCT ACTTGGTCTT CTGCACTTTT GTCTCTGACG TACTTCCTTT      60
CTTCACAAGT GCCATTACA GAAAGCTGGG CTAAACCAT TCCCAGCTAT TCCTCCTACA      120
GCTTTCCTGA ATTATTTCAG AATACAAAAT TCTGTATCTC CAAGAACTA TTACAGATTT      180
AGATTTAAAA ATATGCACTA TTTCTACCT TGTATGTTTT GCTTACTATT TTTTTCGTC      240
AGAGGATATG TCTTAAAAAT TGAAATGCAT CAAAAAT                                277

```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

GAATTCGGCC TTCATGGCCT ACCAAGTCAA AAAATAGAAC AGTTCGGCA CCCCAGAAGC      60
CCTTTGCCAC GTGGTCACAA CCTCCCTGT TTCCACCAAC AGTAACATTC TAGTTTTTAC      120
AGTAATTCT TCCTTGCTTT TCTTTGTAAT TTTACTGCCC TGTGTTTCTT AATATGATTT      180
AGTTTGCCT GGTTCCTT TCATATAAAT GAAATCATAC TGAATATATT ATTCATATT      240
TTGCCAATA TTTGTTGT AAGATTCATC CATCTGTAG CTCCAATGTA TTTATTTCA      300
TTTTGTATA ATTATATGAT TATGCCACAG TTTGTCAGTT CACTCGAG                    348

```

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GAATTCGGCC	TTCATGGCCT	AGAATTATTA	GGAAACAAAT	GGTTTTGCTG	TCTTTTGGTC	60
ATTAGCTTGG	CCCCATGTTT	AAGCATTCGG	TAACAACGTG	GAAGAGCCTG	CTACAAATAA	120
AGTGGTAGGT	GCTCTGAAGA	AAAATAAAGC	TGTTAAAGGG	AATAGAAAGT	GATGAAGGCA	180
GGGGCTGTTA	GACAGGCTGG	TCAGTGTCTG	AGGAAGTAGC	CCTGCACTGA	GACCTGAAAA	240
GTAAAGAAGC	AAGCCATGGG	GAGTTGGGGA	GGAGCATTCC	AGACAGAGGC	TTGATGTGTT	300
GAACCATCTT	TTCCAAGCTC	TTCTCTGTG	ACCTTCTCTT	TAGTCACTAT	GTCCCCTTTC	360
TATCCAGAC	CATAATTCCA	CCATTTATCT	TAAGGCTGAG			400

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GAACGATTGA	ATTCTAGACC	TGCCTCGAGA	TCAGCACTAA	CCCCCCAAC	TCCCAGCCTT	60
TAGTTTGCTG	TAGGCTGTCA	AACCAGATAA	CCAAACTTGT	TAAATTGAGA	ATCAATAGGC	120
TGTACATAGG	GACTACAACA	GAATGACGCT	CATTATTGAC	AGAATCAAGT	TCAAAGTCCT	180
TGTCCTGGCG	TCTGTTGGCC	TCTGGCAGCT	GGCTCATCTG	GCATTAGCTG	GTTGCACGAG	240
TTGCTGCAAC	CCTCCCACCC	CGCTCGAG				268

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GTGAGGTTTT	AACTGAGCTC	GAAGAATTGG	AATCAAAAGA	GATAGGTTTG	TCTCAGTCCA	60
GACAGTGGAT	AGCATAAGGA	AAGTACAAC	GCAGAAAAGA	GGGGGACAGC	GAAGAGACTG	120
GATTGATGCG	TTATCTAGGC	GGTACCTGTC	TCCATTCTTT	TCTAGCCAGC	CTTTGAGCAT	180
TTATCAAGA	ATAGAGGAAT	TCAAAGTACT	GCAGTCTGCT	TGAACCAGTG	CTTGTGAGTG	240
GCTCTAAAAA	AAATACTTGA	ATTTGAACTT	GAAAGAACAC	TCAAATAAGG	TTTGGGGCTT	300
CTCTTTGTTT	AATACTTTAA	GCGTCTTATT	TCTAACATAA	ATATACTGAT	TGCACAGAAT	360
TTGATTGTTC	ATAGCAGCAG	TTGCCTGTAC	TTTAGAATTC	TCAGATATTA	GAGCTGAAAG	420
ATCATCTGAG	TTACTTTATA	AATGGGGAAA	TCTCGATCTC	GAG		463

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAACGGCAGC	CATTGAAGCA	TATTGGAAAA	GGAAGTGGGG	AATTTATTAA	AGCACTCATG	60
AAGGAAATTC	CAGCGCTGCT	TCATCTTCCA	GTGCTGATAA	TTATGGCATT	AGCCATCCTG	120
AGTTTCTGCT	ATGGTGCTGG	AAAATCAGTT	CATGTGCTGA	GACATATAGG	CGGTCCTTGA	180
GAGAGAACCT	CCCCAGGCAC	TTCGGCCACG	GGATAGAAGA	CGGCAGGAGG	AAATTGATTA	240
TAGACCTGAT	GGTGGAGCAG	GTGATGCCGA	TTTCCATTAT	AGGGGCCAAA	TGGGCCCCAC	300
TGAGCAAGGC	CCTTATGCCA	AAACGTATGA	GGGTAGAAGA	GAGATTTTGA	GAGAGAGAGA	360
TGTTGACTTG	AGATTTTACA	CTGGCAACAA	GAGCCCTGAA	GTGCTCCGGG	CATTTGATGT	420
ACCAGACGCA	GAGGCACGAG	AGCCCTCGA	G			451

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GAATTCGGCT	TCATGGCCTA	CTCAGATCTT	AAAATTCAGG	CTGTCAAAGA	GATTTCCTAT	60
GAGGTTGCTC	TCAATGACTT	CAGGCACAGT	CGGCAGGAGA	TTGAAGCCCT	GGCCATTGTC	120
AAATGAAGG	AGCTTTGTGC	CATGTTNTGC	AAGAAAGACC	CCAATGAGCG	GGACTCCTGG	180
AGGGCAGTGG	CCAGGGACGT	CTGGGATACC	GTCCGTTGTT	GGGATGAGAA	GATCGAAGAC	240
GTCTGGGCA	CTGGGAAAGG	CAGCACTGAT	GTAGATGACC	TCAAGGTTCA	TATAGACAAG	300
CTGGAAGATA	TTTTGCAAGA	AGTCAAAAAG	CAAAATAACA	TGAAAGACGA	GGAGATAAAA	360
GTCTTAAGAA	ATAAAATGCT	CAAAATGGAA	AAAGTCTTGC	CACTGATCGG	ATCTCAGGAA	420
CAGAAAAGCC	CAGGAAGCCA	CAAAGCAAAG	GAGCCTGTG	GTGCTGGTGT	TAGTAGCACC	480
TCTGAGAATA	ATGTAAGTAA	AGGAGACCTC	GAG			513

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CAGAATGGGA	TCGAAGCCTG	CCTCCTTAGG	NTCTTTGCCN	TCATCCTCTC	TGGCAAATGC	60
AGTTACAGCC	CGGAGCCCGA	CCAGCGGAGG	ACGCTGCCCC	CAGGCTGGGT	GTCCCTGGGC	120
CGTGCGGACC	CTGAGGAAGA	GCTGAGTCTC	ACCTTTGCCC	TGAGACAGCA	GAATGTGGAA	180
AGACTCTCGG	AGCTGGTGCA	GGCTGTGTCG	GATCCAGCT	CTCCTCAATA	CGGAAAATAC	240
CTGACCCTAG	AGAATGTGGC	TGATCTGGTG	AGGCCATCCC	CACTGACCCT	CCACACGCTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

GAATTCGGCC TTCATGGCCT ACTTCATTGT AAGGTACTTC TTTGCGGCGC TGACAGTGCT      60
CACGCTCCTG GGCCTCCTCC ATGGACTCGT GCTGCTGCCT GTGCTGCTGT CCATCCTGGG      120
CCCGCCGCCA GAGGTGATAC AGATGTACAA GGAAAGCCCA GAGATCCTGA GTCCACCAGC      180
TCCACAGGGA GCGGGGCTTA GGTGGGGGGC ATCCTCCTCC CTGCCCCAGA GCTTTGCCAG      240
AGTGACTACC TCCATGACCG TGGCCATCCA CCCACCCCCC CTGCCTGGTG CCTACATCCA      300
TCCAGCCCCT GATGAGCCCC CCAGGTCCCT CGAG                                     334

```

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

```

GGATTTTAAG GATCACATTC CAAGGGAAC TGATATGAAG GTTGCAATGA ATGTGTATGA      60
GTTATCATCA GCTGCCGGAT TACCTTGTGA GATTGATCCT GCATTGGTCG TAGCTCTTTC      120
TTCACAAAAA TCGGAAAACA TTAGTCCAGA AGAAGAGTAT AAAATTGCCT GCCTTCTCAT      180
GGTGTTTGTG GCAGTTTCTT TGCCAACACT GGCCAGTAAT GTGATGTCTC AGTACAGCCC      240
TGCTATAGAA GGGCATTGCA ACAACATACA TTGCTTGGCC AAAGCCATCA ACCAGATTGC      300
TCGAG                                     305

```

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

GAATTCGGCC TTCATGGCCT ACCCAAACAT TATCCCTCTA CACTGTCCCC ACTATGCTAT      60
ACCCCTGCAC TATACCCCTA TGCTGTCTCC CTTACGCTAT CCCCCTATGC TATGTCCCCT      120
ACACTATCCC CCTTTGTTGT CCCTCCATGC TACTCCCTAC GCTATCCCAC TACTCTATCC      180
CCCTGACGCT GTCCCCCTAC GCTATCCCGC TACACTGTTC CCCCTACACT ATCTCCATAC      240
ACTGTCCCCC TACACTCTCC CCCTACTCAA TTCCCCCTAC ACTCTCCGCG TACACTATCC      300
CCGCTACACT ATCCCCGAC GCTCTCGAG                                     329

```

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GTTCGAATGC TCTTTACTTC CTTTGTGGAG CCTCCCTGCA CAAGCAGCAC TTCTTTTTCG	60
CATAGCAACA TGTGCATCAA TAATTCCTTTA GTCTGTAATG GTGTCCAAAA TTGTGCATAC	120
CCTTGGGATG AAAATCATTG TAAAGAAAAG AAAAAAGCAG GAGTATTTGA ACAAATCACT	180
AAGACTCATG GAACAATTAT TGGCATTACT TCAGGGATTG TCTTGGTCCT TCTCATTATT	240
TCTATTTTAG TACAAGTGAA ACAGCATCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GAATTCGGCC TTCATGGCCT ACATAACTCT CCACAGGCTC CCCTGGGAGG GGTGCCCCCA	60
CCTCACCCGC CACCTCACTT CTCAGCCCCT CTTCCCATCC AAGGGCTCCC TGGGCTGCCC	120
CCACCCTAGT CATGATCTCG CTCCTCTACT CTCTCGTAGT ACTTTATTTT TACCTTGCTC	180
CTGGCTCACA TTACATGCTT ATCTTGTTAT TATAGATGGT TCTACATATG TCTCCTTTTG	240
CATCCTTTTC TCAAAGCTCC TGTGAGGCCA GGGATGGTTT TATGCCTTTT CTCATCCCTT	300
TATGTTCTAG TATAATGCTT TACACATGTT TACTCGAG	338

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GAATTCGGCC TTCATGGCCT ACTTTCTCTC CTTTTTCCT GTAAGTGTGC TGGTTTGTGTT	60
TTGGTCTTCC TCTCATACCC GTTCTGTCAT TTCATCTTTT CTTTCTATTG GGACTTCATT	120
TCATTTTTTT TTAACCTTAT CTTTGTGTTT TCTTGTTTAT CCCATCCTTT TTGATAAAAT	180
CCATCGCATG TGTCTTCTTT TTTTCTTTAT TTTCTTTCCT TTCCTTTTTC CTTTTTCTTT	240
CTCCCAAAT TTTTCTTTT CACAGCATTG GAACACGGGA GGTAGTCACC CAGAAGAACT	300
TGAGCGGCCT GGTGCCCATC CGAGACCACT CGAG	334

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

GCAGAAAATA TGGTATCGGT TTCATTTAAT AAAAATGAAA AAATAATTTT CAGTTATCAG      60
TAATTTCTCA GTTACACAAC CTCTGCCTTC ATTTCCGCTT AGCCATGAAC TTTTACTGCG      120
ACAAAGGAAT TTTAAATAGC CAAATCTAC  AATTCTGGCT GGGTGTGGGG GCTCATGCCT      180
GGGATCTCAG TAGTATGGGA CCCCAGGCA  GGTCTAGAAT TCAATCCTCG AG                232

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

GCCTCTGCTT TTAATTCATT GGCAACTGTT ACGATGGAAG ACCTGATTCT ACCTTGGTTC      60
CCTGAGTTCT CTGAAGCCCG GGCCATCATG CTTTCCAGAG GCCTTGCCTT TGGCTATGGG      120
CTGCTTTGTC TAGGAATGGC CTATATTTCC TCCCAGATGG GACCTGTGCT GCAGGCAGCA      180
ATCAGCATCT TTGGCATGGT TGGGGGACCG CTGCTGGGAC TCTTCTGCCT TGGAAATGTT      240
TTTCCATGTG CTAACCTCC TGGTGTCTGT GTGGGCCTGT TGGCTGGGCT CGTCATGGCC      300
TTCTGGATTG GCATCGGGAG CATCGTGACC AGCATGGGCT TCAGCATGCC ACCCTCTCCC      360
TCTAATGGGT CCAGCTTCTC CCTGCCACC AATCTAACCG TTGCCACTGT GACCACACTT      420
CTCGAG                                         426

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```

GAATTCGGCC TTCATGGCCT AGGCCCTTAA ACTGGATTCA AAAAATGCTC TAAACATAGG      60
AATGGTTGAA GAGGTCTTGC AGTCTTCAGA TGAAACTAAA TCTCTAGAAG AGGCACAAGA      120
ATGGCTAAAG CAATTCATCC AAGGGCCACC GGAAGTAATT AGAGCTTTGA AAAAATCTGT      180
TTGTTCAGGC AGAGAGCTAT ATTGGAGGA AGCATTACAG AACGAAAGAG ATCTTTTAGG      240
AACAGTTTGG GGTGGGCCTG CAAATTTAGA GGCTACCTCG AG                282

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

GATTGAATTC TAGACCTGCC TCGAAGGCCG AGAGGGGAAAG TTGAAAGGTC CCAAATTCAA      60
GATGCCTGAG ATGAACATCA AAGCCCCCAA GATCTCCATG CCTGACATTG ATCTTAACCT      120
GAAAGGACCC AAAGTGAAGG GTGATATGGA TGTGTCTCTG CCAAAAGTGG AAGGTGACAT      180
GCAAGTTCCT GACTTGGATA TTAAGGCCC CAAAGTGGAT ATTAATGCCC CAGATGTGGA      240
TGGACTCGAG                                     250

```

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```

GAATTCTAGA CCCACCTCCA CCTTTAACTC GAAGTAACAC TGCAAATCGT TTAATGAAAA      60
CACTCTCAAA ACTGAATTTA TGTGTTGATA AACAGAGAA AGGAGAAAGT AGTAGTCCTT      120
CTCCATCAGC TGAAAAGGA AAGATTCTAA ATGTTTCAGT GATTGAAGAA AGTGGCAATA      180
AAAACGATCA AAAGTCTCAA AAAATTATGA AGAAGAAAGA GTCATCTTCT ATGTTGGCTA      240
CAGTTAAAGA AGAAGTCTCT GGTAGTTCAG CAGCTGTTAC GGAGAATGCT GATAGTGATA      300
GAATTCTGA TGAAGCAAAT AGTAATTTTA ACCAAGGGCT CGAG                          344

```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```

GGAGTAATCA GAGGTGTTCT TGTGTTGTGA TAAGGGTGGC AGGAGTGGAC ATTCTTCACA      60
TACACCCATT ATTGTTTGA AGTGTTTAAT TACCTTTTGA GCTACATTTT TGCAGCTGAG      120
TTTAGAATGA AAACCACAAG AGTTTTATTG TTGGCTGTAC TCGAG                          165

```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```

GAATTCGGCC TTCATGGCCT AGAACAGAGC TTACTTATTC TTTCTGAAAC CAAGGCTTCT      60
CTAGTGAGCA CCATGAGCCT TTGGAACAA CAGATGTATA CAATAGCAAA GTTTCATTTC      120
TTTACCTTGA AACGTGAAAG TAAATCAGTG AGATCAGTGT TGCTTCTGCT TTTAATTTTT      180
TTCACAGTTC AGATTTTTAT GTTTTGGTT CATCACTCTT TAAAAATGC TGTGGTTCCC      240
ATCAAACG AG                                     252

```

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

GAATTCGGCC TTCATGGCCT AGGATGTTCA CTTGCATGCC TCTGGATTTT AAAATTATTG      60
TTCACATGAC TCCTTTTCTG TCGTTGGGA AGCAGCTACA GAGCAGTAGA ATCCACTGAA      120
TTGGTACACT GAAGCAGGCA TGCCATTAA ATGAAGGCAG TTAACCTTGA CTGTTGTATC      180
ACCAGAGTTA AAGAATTCTG GTGCCCCCTCT TTAAGTCTTC AGGAAGTGTT TAGAGGCTTA      240
TTCACATTAG TTAAACACAGG CCCCCCCCAC CTTCCCCAAG GCAACAGAAA ACATAACCAT      300
TAGCTCTCTT CCTGTTTTC TCCCTCATTT CATGCTTGCT TCGGCTGCTA AACTGAATTT      360
TTGTTACTTA GAATATTATA AAGTGTGGAT GCTTTCTATA ATGCTATTGG TCTAAGTGTG      420
ATTAAATTTC ATTAAGGTGT ATAAGCCTCT AATTATTACA TAACTGGCAC TGGCTCGAG      479

```

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

GAATTCGGCC TTCATGGCCT AGCCTATTAC ACAGTAAGTT AATAATTGTG TCCTTGCAAA      60
TAAGCATTGT GTTCTGAAAT GGAATCAGCA TATTTCCCTA TAAAGACACT TCCACTCATT      120
CATTAAATGA GCAGCCCCAG TTGATAAAGA ATCAGTATAT CATGTTCTGA TATTTAATCA      180
GCAAACATCAT TTATTCAGTA GAAATTTGAA TTCCTGTGAT GTGCCAGGCT TGTGAGGAGG      240
GAGACTCGAG                                     250

```

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

GAATTCGGCC TTCATGGCCT AGTCGACTCC TGTGAGGTAT GGTGCTGGGT GCAGATGCAG      60
TGTGGCTCTG GATAGCACCT TATGGACAGT TGTGTCCCCA AGGAAGGATG AGAATAGCTA      120
CTGAAGTCCT AAAGAGCAAG CCTAACTCAA GCCATTGGCA CACAGGCATT AGACAGAAAG      180
CTGGAAGTTG AAATGGTGGA GTCCAACTTG CCTGGACCAG CTTAATGGTT CTGCTCCTGG      240
TAACGTTTTT ATCCATGGAT GACTTGCTTG GGTATGGAGA GTCGGCTTGA CTACACTGTG      300
TGGAGCAAGT TTAAAGAAG CAAAGGAACT CCTCGAG                                     337

```

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

```

GCGATTGAAC TCCTGACCTC AAGTGATCTG CCCACTTGTG CCTCCCAGAA CTGGGATAAA      60
AAAAAAAAAA ATAGATCCTT GGTATTATTC CATTACATAC GGATTGTAAA ATTCAGTTAA      120
ACATTCATCT CTTGGTGGGC ATTTATGTAT TTCTTTTGTT TGTGTTGTTT CAGCATTGCT      180
CTGTAAACC TTTTATAAG TACATCTCGA CTCGAG                                     216

```

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

```

GAATTCGGCC TTCATGGCCT ACCACATTG TAACGGAGCC ATTGAAGCAT ATTGGAAAAG      60
GAACTGGGGA ATTTATTAAA GCACTCATGA AGGAAATTC AGCGTGCTT CATCTTCCAG      120
TGCTGATAAT TATGGCATTG GCCATCCTGA GTTCTGCTA TGGTGCTGGA AAATCAGTTC      180
ATGTGCTGAG ACATATAGGC GGTCTGAGA GCGAACCTCC CCAGGCACTT CGGCCTGGGA      240
TACTCGAG                                     248

```

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

```

GAATTCGGCC TTCATGGCCT AGCCTTCCTC TACCATTTT AATTTTTTTA GACTTCATTT      60
TGTGATTTAT TGCTGCTCTG GGGGCTTCAC ATCCAATCCT TTTATGTTT CATCTTTCCT      120
TTCCTTACAT TTGTTGCATA TAACAATGGC GTGTTTAGCT ACTGCAGTGA AAAATCAATC      180
AAGCCTATTC CATATTCACA GGCTTGCAAT GGCACCAACG GCTCCTGGAT CTCTCGAG      238

```

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```

GAATTCGGCC TTCATGGCCT AAGTTGATCC GGATACACAC CTGCTAAAAC TGCTTAAAC      60
ATTAGAAGGA CATGCTTATG GCGTTTCTTA TATTGCATGG AGTCCAGATG ACAACTATCT      120
TGTGCTTGT  GGCCAGATG ACTGCTCTGA GCTTTGGCTT TCGAATGTAC AAACAGGAGT      180
CTCTCGAG                                         188

```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

```

GAATTCGGCC TTCATGGCCT ACAGGCATGT TCAGATTTCG AAAAGTGGAT GTAAGTAA      60
TTCAGATAGC TTTAGTGATT GTCTTTGTGT TSTCTGCATT TGGAGGAGCA ACAATGTGGG      120
ACTATACGAT TCCTATTCTA GAAATAAAAT TGAAGATCCT TCCAGTTCTT GGATTCTAG      180
GTGGAGTAAT ATTTTCCTGT TCAAATTATT TCCATGTTAT CCTCCATGGT GGTGTTGGCA      240
AGAATGGATC CACTATAGCA GGCACCACTG TCTTGTCACT TGGACTCCAC ATAGGACTAA      300
TTATTATACT GGCAATAATG ATCTATAAAA AGTCAGCAAC TGATGTGTTT GAAAAGCATC      360
CTTGTCTTTA TATCCTAATG TTTGGATGTG TCTTTGCTAA AGTCTCACA AAATTAGTGG      420
TAGCTCACAT GACCAAAAGT GAACTATATC TTCAAGACAC TGTCTTTTTG GGGCCAGGGC      480
TCGAG                                         485

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```

GAATTCGGCC TTCATGCCTA GTGGATCCGG AACTCTGTG GCTCTAGACT TTCAACTATT      60
TTATTTTTTC TTTTGTATTT TTTGTTTGT TCTTGCTTTT TTACAATGGG AACTAGAATG      120
TAAGATGCCA AACTCAGCCT GTGGGGAACA TGGATTTTCA CAACAGCAAC CACAGAGCGT      180
GGTTTCCATT TCTATTCCT GTTCATGTGG GAGGCAGAGA AGGAAATCAG GTGCTCAGTT      240
CCAGGGACAT CACAGGACAG GACTCGAG                                         268

```

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

GAATTCGGCC TTCATGGCCT ACACCTCTTC TGCCAACCAG CTGCTTGGGA TGA CTGCGAT      60
CCCGTGTGCT TGTCTGGGTA TCTTCCTGGG AGGTCTTTTG GTGAAGAAGC TCAGCCTGTC      120
TGCCCTGGGG GCCATTCCGA TGGCCATGCT CGTCAACCTG GTGTCCACTG CTTGCTACGT      180
CTCCTTCCTC TTCCTGGGCT GCGACACTGG CCTGTGGGCT GGGGTTACTG TTCCCTATGG      240
AAACAGCACA GCACCTGGCT CAGCCCTGGA CCCCTACTCG CCCAAG      286

```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

GAATTCGGCC TTCATGGCCT ACCTGCCTCG AGATGATCAT TCTTTTCTTG CTTCTAGGCT      60
CTGTGTCCTC CTGGTTTCCT CCAACCTCTC TGGTCCTGTT TCATTGCTG TGGGTTCTCT      120
TTGCCTTTGC CACCCCTCAA ATGGGGCTTC TACTCAGCAC TAGTGAGTTT TCAGTGCTTG      180
CAGACCCAAC ACCCTCTTTT TATAACAAAT ATTTTTTAAT ACGTCCTTTT CCACAACCTG      240
AG

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

GAATTCGGCC TTCATGGCCT AGTCCCATCA GAGGGAGCTG ATGAAGAATG GTCCCTGTAA      60
GTAAGTCACT AGGTTCACCA ACTGCCTGGC CGAGCACTCA GCCCGTGGAG CTCAGGCCAA      120
CACCAGAGCC CCGGTTTGTAG GGGCCAGGAG AGCAGGTGAC CAATTATTTG GGGAGTCTTG      180
GGTAGAATTT CCGCCACACA TTCTCCCAG GGTGTCAGGG GTCTCCGAG GCAGGGCGGT      240
GGAGCAGGAT TCAGGATGTG GTGGGAATAG AGTGAGGGGC AGTGGGTGCT GCTCGAG      297

```

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

```

GAATTCGGCC TTCATGGCCT AAAAACTAG AATAATGGAA GAGTAAATAA ACACAATTCT      60
TAATGTATTA CAAGAAATAA AAGGTTTAAA AGTAGATTTT TTAATTGAAA AGAATTAAAT      120
CAGATAAAAA TATTGAGAG GTAATGCAAA CATTTAAGTT TGTCAAAGAA GCITCAACAT      180
CTGGATAATA GGAAAGAAAA AAACCAAGC AAAAGAAAAA TAAGCCACAA ACTAAAAAAT      240
GTTTAGTTCT TGAAATTTAA AAAAGTAAAT ATTGAAAGAG CATGCTGTGT ACCTGAGATT      300

```

ATTTACCCAA AACTCGAG

318

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GAATTCGGCC TTCATGGCCT AGATTGAATT CTAGACCTGC CTCGAGTCTG GGCACCCCTGA	60
GCAGCAGCCT GAGCCGGGCC AAGTCTGAGC CCTTCCGCAT TTCTCCGGTC AACCGCATGT	120
ATGCCATCTG CCGCAGCTAC CCAGGGCTGC TGATCGTGCC CCAGAGTGTC CAGGACAACG	180
CCCTGCAGCG CGTGTCCCGC TGCTATCGCC AGAACCGCTT CCCCCTGGTC TGCTGGCGCA	240
GCGGGCGGTC CAAGGCGGTG CTGCTGCGCT CTGGAGGCCT GCATGGCAAA GGTGTCGTCG	300
GCCTCTTCAA GGCCAGAAC GCACCTTCTC CAGGCCAGTC CCAGGCGGAC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GAATTCGGCC TTCATGGCCT AGTCATGGAA CAAGTCCTTG CTAAACTAGA AAACAGGACT	60
AGTATTACTG AAACAGATGA ACAAATGCAA GCATATGATC ACCTTTTATA TGAAACACCT	120
TATGAAACCC CACAAGATGA GGGTTATGAT GGTCCAGCCT GGGTGACAGA GCGAGACTCT	180
GTCTTATAAA GAAAAAAAAA AAAAGAAGTG GCAGCTCTGT CTGCTTCTCA CAGAGTTGCT	240
AGGGACAACCT GCTGAGGCAG GCACCTGCCC TTGGGCTCCC CGGGTGGGCT GCTATTGCCC	300
TGTGGGCTCT GCCTGCCCCG CTGTCCAGTC CCCGGGGTGG CTCGAG	346

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCGATTGAAT TCTAGACCTG CCTCGAGAAC AGGGAACCTT CAAACAAAAG ATATATCATA	60
GGAAGTCAGG TGAGAAGCTG TCAACTGGGC AGGCAGTGAT GAGAATCGTA GTTGTCTTAC	120
TGTACTTTTT TGTTTTGTTC AAAAACCTA AAGCATCAGC CATTTTGAAA GCAGAGTTTG	180
CAGAGAGCCC CCAACAGAGC CAGAACTTGC CAAGAGCGAC TGATATTCTT AGAATCCAC	240
GAGGCAG	247

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

GAATTCGGCC TTCATGGCCT ACAACATCAA AACTCCCAAG CAAATGGATG AATTCATTGA      60
GATCCAAAGT TCAACAGGAA CCTGGTACCA GCGCTGGCTG GTCAGATTCA AGACCATTTT      120
CAAGCAGGTC TGGGATAATG CCCTGTACTG TGTGATGGGG CCCTACAGAA TGAATACACT      180
GATTCTGGCC GTGGTTTGGT TTGCCATGGC ATTCAGTTAC TATGGACTGA CAGTTTGTT      240
TCCTGATATG ATCCGCTATT TTCAAGATGA AGAATACAAG TCTAAAATGA AGGTGTTTTT      300
TGGTGAGCAT GTGTACGGCG CCACAATCAA CTTACAGATG GAAAATCAGA TCCACCAACA      360
TGGGCCTCGA CCTGACTTTG CCCCCTTGCC CATCAGCCAT TTGCCATCAC CCCAAACAAC      420
TCAGCTTCGG GGAAGTCTCG AG

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

CCGAGTGACC TTCTTGATGC TGGCTGTTTC TCTCACCGTT CCCCTGCTTG GAGCCATGAT      60
GCTGCTGGAA TCTCCTATAG ATCCACAGCC TCTCAGCTTC AAAGAACCCC CGCTCTTGCT      120
TGGTGTTCTG CATCCAAATG CGAAGCTCCT CGAG

```

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

```

GAATTCGGCC TTCATGGCCT AGTTTACTTC TGCTTGATCT TTATTCTTCC TTGCTACTAA      60
TTTTGGATTT AGTTTGTTCT TTCTAGACA TTCATTGTGA GATTGTTTAT TTACAATTTT      120
TCTAGTTTTT TTGATGTAGA CATTTA

```

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

```
GAATTCGGCC TTCATGGCCT AGATGTTGCC AGTTTTCATG GAGGAAGTAG ACATGAAAGC    60
TTGTTTGTAA TGTGTTTGAC AGAGTAGAAA GACATTGAAG AAGGTGATGG TATACATCAC    120
TTGAATATTT TTATTGAAAA GGGAGGGAGG AAATGGAGCG TTAGTTGTAG GACCAGATGA    180
TGTAAGAGA GTTTTTTAAA GTGTACAAAA CAATGGCATG TTGTGATACT AATGAGAAGG    240
AGCCAATAGA GAACAAAAAA TTGATGATGC AGGAGACGAC TCGAG                    285
```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```
CTCGAGGGAT CTGGCTTTCT CTGTCTTCTC ATTTACTACA TNACGCTGGT GAATTAATAG    60
ATNTCTCAAC AAAAGGACAT TTAAATCAAC ATATGACACC TGTTTAAATT CTTAAGAAGC    120
CATTAATTAC ACATTCTTAA GAAATGAGC TATGACACAA CTCTTCTCAC TGTATAACTC    180
CTATCTGTGA TTCTCAATCA GGTGACTTTT CAGCTNCAAG ACGGATCTTT TCTATTCATC    240
TCCTCTGGTT CGGACCAATT AAATGNTTC TTTTGCAATC ANAACATCTC ANNTGCCAAA    300
TCTTCAAAG CAAAGGAGTT NGTTAGCAAC ATATTAGGCC ATGAAGGCCG AATTC        355
```

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```
GAATTCTAGA CCTGCCTCTG TATGTTGCTT TAGCCAGGAT TCAGAGCTAA AGTGTAAGTG    60
TGTGCTTCTG CTTTCTGGAT GTATCTCTCA AAATGCTCT GTCTGTTTAT TCAGCTCCTG    120
GATCTACCTT CTCTTTCTT TGAATGGAC ACCATTCTAT TCATTGCTCA CTCAGAACTT    180
CAGCTGTTCT CATGATCACA TGCTTCTTC CCTGTTTATG TCCAAT                    226
```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

GAATTCGGCC TTCATGGCCT AGTCTGCTGC TTAGCTTGTA TTTTCAGTTT AATATATTCG      60
TGATCATTAA CAAAACAGCG AAGTGAATAA TGGGCATAAA TTTTCCTAAG AAGAATCATT      120
TTCCATACTT ATTTTCAAT ATTATCAAAA AGTATGTAAT TTGGGGGGT TTTTGGTTT      180
TTTTTTTTT TGAAACAGAA TCCTGCTCTG TTCTCGAG      240

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

GAATTCGGCC TTCATGGCCT ACTTTGAACA ATTCGGCATG AATTGAAACC AGGTTTTCCT      60
GTGGAAAGTT ATAGCTTGAT TGGGAGATAG AAGTTGAATT GAGTTCCTTC TTGCAACTCT      120
TAGTGTTTAT TTTTATATCT CAGTAAGACG AGGATACCTT CAGTTTGAAT CTCGATAATG      180
TTCCTGCCA AACTCCTTCT CATTAAATGC TTATGGCCTT CACATTTCTG TATAATAAAG      240
ATCAATTATC AGCACTCGAG      260

```

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

GAATTCGGCC TTCATGGCCT AAGCATATGA ATTTTGGAGA GACAGACATA CAGACCATAA      60
CAGTTCTATT TTCTATAACT ATAGTAGAAT ATCGAAATGA GAACATTGAC ATTGGTAAAA      120
GGTGTATGTA TAGTTTATAT GTTATCTTAT CAAAAGGGTA GATTACAGA ACCAACACAA      180
GTAAGCTATA GAACTAGCCC ATTACCACAA AGATCTCCCA CAAGCTACAG CTTTACAGTC      240
ATACCCACCC GGCTCGAG      258

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

GAGGACCTTT ATAATCTACT ACTAATTACT GTGAAAGTAA ACATTGTTTA ATATACCAGT      60
TCTTAAAGAA ATATTTTGTC TAGTCATTAA TATTCTAGTT CATCTCAAAG CTTCATTG      120
ACAATTTAAA ATTACTTAAA TTTTAATATT AAAGGAAACA GTTTTCCTGA TTCTCATGAA      180
AGTTCCTATT TGCACTGAAG ATGACTAAAC CTTTGTAGTCA TAGTTTTAGA AGAATTGGCT      240
TTTTTATAGC CATTTTATTT ACATATGGGT ACGGACTCGA G      281

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```
GAATTCGGCC TTCATGGCCT ACTCAGAAAA GAAATGAAA ATACCTCTAC ATGTGGTCTT      60
CCTGCTAATC TCTCTGACCT TCCTATTCAC CACCCTCCCC ACTGCCCACT TACTCGAG      118
```

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```
GCGAGGATGG CATGGACGCT TATCGAGCAG CTTCAGGGTG GCAGCTACAA GAAGATTGGC      60
TACTATGACA GCACCAAGGA TGATCTTTCC TGGTCCAAAA CAGATAAATG GATTGGAGGG      120
TCCCCCCCAG CTGACCAGAC CCTGGTCATC AAGACATTCC GCTTCCTGTC ACAGAACTC      180
TTTATCTCCG TCTCAGTTCT CTCCAGCCTG GGCATTGTCC TAGCTGTGTG CTGTCTGTCC      240
TTTAACATCT ACAACTCACA TGCCGTCTC GAG                                273
```

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

```
GAATTCGGCC TTCATGGCCT AAGCAGTTGC TAATGCCAGC AGTACATAAA TTGAGGATGG      60
AGCAAAAGGA TCGACACCAC CAATGGCTGC ATTGTGATAG GTGTGGACAG AGCCTGCCAG      120
AATTAAACAC ACGCCAGGAC TCGAG                                145
```

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

GGATTCGGCC TTCATGGCCT AGTGTTTATA ATTAATCCTT TAATATTATG GTTATTAACC      60
TCTTAAACAT GAATGAATTC TTGATTGTTT TAACACAGTA CCTAAGACTA ATGCTTTCTG      120
TGGACACCAC TGAGCTCTGC CTCAACTCCA CCCTCTGCGA CCGGAGGACT ATGCCCTAG      180
TAACTGCTGT CCGTGTGGAC GCTGTGCTGG TTCTGTTTTC TAAAGGAGCA GAAGGACAGG      240
TCTCTGAGAC AGGATCGTTG TCCCTACAGG AGGAACAGTG GCCACTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

```

GCGATTGAAT TCTAGACCTG CCTCGAGCCT CCCAAAGTGC TGTGATTACA GGAGTGAGCT      60
GCCACGCCCA GCCTACAAGT TTTTCTTTAA CTACTGCTTT AGTCAACCAT ATCCTCTAGC      120
TTCTGATATT TTCATTGTTT GTTGTCATTT TCTAGATATT CAACAATTTT AAATTAGATT      180
TTCTCTTCGA CTAAAGTGGA AGAATTTTTT CCGTTTATT TTCTACATGC TAAAGATTTT      240
TATTTTCATT TTGTATTAA TTTCTAGTGT TACCGTATTG TCATTAGAAA ATATGGGCTG      300
GCTCGAG      307

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```

GAATTCTGAA AATATTAAGA TTTATCCTAG CACTTACGTT CAACATACCA TAATTTTAT      60
ACTTCTCCAT CTAAATAAAA CCAAGTTTGT TCCTACACTA GTCCAGCCTG CATTTCTAAG      120
AACTCCAGTG ATTATACATC AACATCTAGA GATCAGGTAT CCCAATCCTT TCTTCCTATA      180
TCTAAGCTAA CTCCTTCTTA GCCAAATGGT ACCCTTTGAT TTTGTGTTAA TCCTTTCCTT      240
CCCTCCACTC TTAACCCCTC TCATTCCATC TTCTCCCTCC CTTTCCACC CCACTCTCGA      300
G      301

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTCGGCC	TTCATGGCCT	AGGTAAAGT	TGTCTGGTAA	TAAGGTGGAG	TGGATTGGG	60
GCAGGTTT	TGTTGTGTG	CTTCTCTTAG	AAGTCAAAGA	GTTGGTGAGG	TAAGTGAAT	120
CCTGTCTATA	TCAGTGTAGT	GATAATGCAC	TAGTGTAATG	AAGAATGGAG	CTGCACGTGT	180
GAGGTTTTTC	AAGTCCACAA	AGATCAGGTA	TTGTCTACGG	TCAATAAAGA	TTTTTTTAAA	240
AAACCCTCTT	AACTAAAGAG	AGGTAAGTTC	CTTTTCAAAA	CTCTGAAATT	TACATGTGCT	300
GACTTATAAT	ATGTGTGATC	CTCGCTGCTT	TTCTGATCCC	TGGTGGTTGG	GGTGTGTGTG	360
TGTGTGTGTC	TGTGTGATGG	GCTCTCGAG				389

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GAATTCGGCC	TTCATGGCCT	AATCTTAAGT	GTTTTACATG	CTCTACCTGC	CGGAATCGCC	60
TGGTCCCGGG	AGATCGGTTT	CACTACATCA	ATGGCAGTTT	ATTTTGTGAA	CATGATAGAC	120
CTACAGCTCT	CATCAATGGC	CATTGAATT	CACTTCAGAG	CAATCCACTA	CTGCCAGACC	180
AGAAGGTCTG	CTAAAAGGTC	AGAGTAATGC	AGAATGCCGTG	CCTTCATCTC	AGATTTGTTC	240
ATCACAGGTG	GATCCCATGT	GTCTTCAGTA	GACAAGTCAC	CTTGTAGCT	AGCACCAGTG	300
CCAGCTCCAT	GCCATTGCAC	CTCGAG				326

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCCA	ATCATTTTTA	AATCTAATCT	GAACTTTAAC	60
TGGTTAGTTG	AGTGCATTTT	TATGTGTACT	GATGTATTG	CATTATTCC	TTACCACCTT	120
ATTTTGTGCT	TTTTATGTTT	TTTCTTCCA	CTCTTTTTTT	TTCTTTTGGA	ATCTCGAG	178

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GAATTCGGCC	TTCATGTACA	TAGATCTTCC	TAGTGTGATT	GACAAAGGTG	ACATTGCAA	60
GGCTTTTTCT	TCATCAGATG	CAGGGATCTG	GACTTCATGT	GTATCCTTTT	ATCCACTCCT	120
CCTCGAG						127

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

GAATTCGGCC TTCATGGCCT AGAATTTAAT TGCAGAAAAT TATTCATATT CTTATAATCC      60
TTTAAATGTC TATAGGATTT ATGATGATAT CTCCCCTTCC ATCCTGATTT TTCAAGTTT      120
TTGTTTTTTC TTTTTTCTTA TAAATCTCGG TAAATGTTTA TTAATTTTAT TCATTTTAA      180
AAAGAACCAG CTTTGGTTT CATAAAGTTT TATAATTTT TTGTTTCAC TTTCATTAA      240
TCTACTCTTT ATTATTCCT TCATTTGTT TACTTTGGGT TTGTTTGCC ATTTTTTCC      300
TAGTTTCTTA AGGTGCCAGC TCGAG                                         325

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

GAATTCGGCC TTCATGGCCT AGGCACACAG GCGGGCAGC AACATAAACG GCACCCATTA      60
AAAAGCAAGA CTCGCTCTTG AGACTAAAGG AGAAGTTACC TAAATTTCTG TATAAACTCA      120
GTAATTCATT CACTTTACTA GTATTACATT TATGAAATTC ACCTTGTGG AAAAAGGAGC      180
GGGAGAGGGA TAAGAAATG CCTGTTTCTA GAAACGCTC GAG                                         223

```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```

GAATTCGGCC TTCATGGCCT AAATTCATAC AGAAGACCTT ATTGTGATAA AGTTCAACGG      60
TATAGGTAAA CAACAACAAA AAAACTATCA ACCATAATTT TTTCACCCTA CCAACATTCT      120
CTGAACCTTT CAGTAATATT TTATACACAT GTGCATATTC TGCCTTTTTC ATTTACTATA      180
TCATAAACTT CTTTCTAGAT CATTATTTT CTGCTGCATT TTTTCAGGAT TTATCACCTT      240
TATTTTLAGT TTTAGTTTT GTGAGTGTAC TCTCGAG                                         277

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

AAATGAGCCC	TATCACTGAG	AAATACGTGT	TTCATGATTT	AACTCTGTGT	GTGTGTGTGT	60
GTGTATTTT	TTTTGGTTG	TCTTCAGCTG	ACAGTATGAA	AAATGAAACT	GCTGAAAAAG	120
CTGAGCACCT	GGTCACCCCT	GGCCTTCCAT	TGCTTTGGCC	TTCAGTAAAA	AGCAGCCTCC	180
CTTCTAGGTC	AGGGAACCAT	GCCATTGAGA	CTAGTAACGG	GCGTTCTGGG	CACAGTCCCA	240
CTGTGCACAG	GTTTGAGAGG	ACAAGTTCAT	CAGAAGGAAG	GCAGTCCTTA	GAAGTCACAT	300
ACGTTGAGCC	CCTCGAG					317

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCGGCC	TTCATGGCCT	ACATTGAGAA	AACAGAAAAG	TTTCAAGAAG	CAGGAAGAAA	60
AGACTCACCT	ATGATCCCAA	CACCCAGAGG	TAATAATTTA	CCATTTTGG	TGTATCTTCT	120
TTGTCTTTTC	CTATGTGTTG	CCTTATGTAG	ATATGTAACA	GGTTGTGGTT	TAAACCGAAG	180
CTATACCCAT	TGTTTGAGT	CAGGCAGGTG	CGATAAATTT	GTAGGTGGCT	CACCAGAAAT	240
CTATTTGCAT	GATGAACCTA	CAGGACTCGA	G			271

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GAATCATTTT	TGGTCACCAA	TCTCTCATAT	ACCACTACTG	GATATTTACA	ACATGCTTCA	60
GTGGAGGAGA	AGACACTGCT	GCTTTGCAAA	GATGACCTGG	AATGCCAAAA	GGTCTCTGTT	120
CCGCACTCAT	CTTATTGGAG	TACTTTCTCT	AGTGTTTCTT	TTTGCTATGT	TTTTGTTTTT	180
CAATCATCAT	GACTGGCTGC	CAGGCAGAGC	TGGATTCAAA	GAAAACCCTG	TGACATACAC	240
TTTCCGAGGA	TTTCGGTCAA	CAAAAAGTGA	GACAAACCAC	AGCTCCCTTC	GGAACATTTG	300
GAAAGAAACA	GTCCCTCAAA	CCCTGAGGCC	TCAAACAGCA	ACTCTCGAG		349

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GAATTCGGCC TTCATGGCCT ACCTGGATTT CTCAATTTAT TAAGTTGTAC TTACCTGATG	60
CTGATGATGA TTAAGTGTAT TACACATTGT CTCAGAGCTC ACTCTTGCGG AGGTTGTGGC	120
CTCGAAAAATG CCTGTGTGTC CCTCTGGAAT CTGTCTTTTC AGCTTCATCT CCTCCTCCTC	180
ACCTCCTGCT GTGGTGACA GATACCTATA GGCAGGCTCC ATCTCCTCCT CCCAGCTCC	240
TCCCCTAGTG CACACCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GAATCTAGA CCTGCCTCGA GTCCTACGGG AAACCTCCAG GGTTTTAGGA AGCTGACGAT	60
GCAAGTTTAT CCAAATGGGA ATGATAATAA TCATGTTTAT TATCCTGGGG TGCTTTCTCC	120
ATAGCAAGTA CTCACCTAGG TCCTGTTTAT TAGTCAGTCT TTTAATCTGT ACTGAAATAG	180
GTGCTGTGCG ATCCATGGGG AATGAACTCG AG	212

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GGTTGCAGTG AGCTGAGATC GCACCACTGC ACTCCAGCCT GGGCAACAGA GTGAGACTTC	60
ATCTCCAAAA AAAAAAAAAA AAAAAAAGA CAACCACAAC AAAAACGAAA CACCACCACC	120
AAAAAAGTTT ACTGGTAGAG TCTCCTCTAG ATTGTTTTCT TTTCAATACT TGTTTCATAT	180
TCTCCAAC TG CCTCGTCCC ATAATGTTGG CTGTGCTTTT CTTGTGCTT ACAGTTCATT	240
GCTGGGATGG ATATGGTGAG TTTTCATGTA CATTGACCAA ATACAATCTC GAG	293

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GAATTCGGCC TTCATGGCCT AGGCTTGAAA GGAAATGAGG GAAATTTTCTG TGAGTTTGAG	60
--------------------------------------------------------------------	----

```

GAATGGCAGA CTGGGTATGT GACAAATGAG TGGGTAAATA AGGAAATCTC AGATTGAGAA      120
TCCTGGCAGA TCTTTCAATG GGTAGACTG CAGGAATATT GATTTTAAAG CCAGACTGAA      180
GCAAATTCTA GTGATAAAGG AAGGGGAAAG GCTGGCTGAA TCAAATGTTT TACCAATACT      240
CCTTTTITTA GTATTGAGT TAAAATTCAG ATTANATGCT TGGCTTAGAA GAATGCAAAG      300
CTTCACTGAG CCTAATAATA TGGATCCCAG TGGGTGAGTG GAGGTGAGTT CACTCGAG      358

```

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

GCTCGAGAGA GCTTTTTTTT TTTTTTTTAA ACATTGTATC ATTAATTTAT CACGTGTATC      60
CAAGCTCCTT TGAGTTTCCC TGCCCCATC CCTGTGTCAT TCCAGCCATA TCCAGCTACT      120
CCTTCCATGC TCCCCCATT CTGTGTTCTG ACTCTATTAC TCCCAGTCCA AATCTTGCTC      180
TTCACGTGCT GCACCTTGTG CTCTCCTCTC TCTCAAAAAA TCTACCCAAA TTCCACCCCT      240
CTTCACAGGC CCCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

CAAGCCGGCC ATATTAGAGA GATGGAAATA AAGCTTCCTT AATGTTGTAT ATGTCTTTGA      60
AGTACATCCG TGCATTTTTT TTTAGCATCC AACCATTCTT CCCTTGAGT TCTCGCCCCC      120
TCAAATCACC CTCTCCGTA GCCACCCGA CTAACATCTC AGTCTCTGAA AATGCACAGA      180
GATGCCCTGGC TACCTCGCCC TGCCTCAGC CTCACGGGGC TCAGTCTCTT TTTCTCTTTG      240
GTGCCACCAG GACGGAGCAT GGAGGTCACA GTACCTGCCA CCCTCAACGT CCACTCGAG      299

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

GAATTCCTAC TAAATAATAT TAAGCAGGAA TTTTITAGGT GTTGCTTTTT AGCTCCTTTT      60
TATCAGTTCT GGGAAGCAAA CAGTGCTGCA TCTCCTTGC TCTCATAGAA TTCTGTAATT      120
TTTATACCAC AGGTCTCTGC TAAAAGCGG CATGTGTTTA GAAATTCTAA AAATGAGGGC      180
TCTGAACITTT GTAACGTGCC TGATACGTTT TCCCTTTTTT AATCCCAACC CCCTCGAG      238

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

GAATTCGGCC TTCATGGCCT ACAACTTGCA CTTGCTCCA GCATCACTGG CCTCCTGCTG      60
TTATTTAGGT ATACTAGGCA TTTCTGTTT TAGGGCCTTT GTACCTCCAG TTCCCTCTGT      120
TTGGAATGCT TTTCCCAGAG TAGCCCTGTG GTTAAATCTC TTACTTCCTT TGGGTCGTGT      180
CTCAGATGTT ACTTTCTCAG AGGGTCCCCC AAGCCCCCAT GCACTCGAG                    229

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

GAATTCGGCC TTCATGGCCT AGAGTCTATT AACTATTTT CTGTTATACC CTGCCAGAAA      60
AGAATTTTAA AAGTTAGTTT ATGTTTGTG TAACCATGTT CTTCAGAAATG CAGGTATGTG      120
AGCATCATGG TTTCTGGGTA ATTCTGCTGC TCCTGTCTTT GAAAATGGAG ATACCACTTG      180
CAGCTTATCC CACTGCTGAG TATTCCAGCA TTGGTAGTGG TTTCACTCCA TTGCATCCAT      240
CCAGAACCTT CACACAGGCC TCCCATTAC CCAGCATCCT CGAG                    284

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

GAATTCGGCC TTCATGGCCT AATAAAATAA AAATTGGAAG AATGGCATT TATTACAGTA      60
TAGTTAAGAG ATTGGCTAAG GCAGTAAATA AACTTAGAA ATGCTCAAAT TTATTGTAAA      120
TTGCTTTTAT AATCATGAT ATATAAGCA TGCTACTGCT AATCAATTAG TTTTATGTAT      180
TAAGACCTAT CAGCATGTCT TTTTTTGTAG ATCTGGTTGA CTTAAACATG ATGTTCTCTG      240
TACCATTTAA CATTTTCAAG ACATATTCTC CCCAACTCG AG                    282

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTCGGCC	TTCATGGCCT	ACTCACCTGC	AATCTATTGT	TTATATTGTT	GCTATGTATC	60
TCTATTCTTT	CTGCATCAAA	TAATGAATAG	CTCATTTTGT	GTGCTTCA	AGTATGACAA	120
ATTCTTTCC	AAATGTGATT	CCAGACAGTA	TATCCAAACA	TGTCTTTCTT	TTCCCATTC	180
TGATCATCCT	ACATGTCAAG	CACTGCCAAC	GTTTACTCAA	GAAAGCTTGG	TTAGAACCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GCAAGCACAA	ATCTAACCAT	GAGCTTCAGC	AATCAGCTCA	ATACAGTGCA	CAATCAGGCC	60
AGTGTTCTAG	CTTCCAGTTC	TACTGCAGCA	GCTGCTACTC	TTTCTCTGGC	TAATCAGAT	120
GTCTCACTAC	TAAACTACCA	GTGAGCTTTG	TACCCATCAT	CTGCTGCACC	AGTTCCTGGA	180
GTTGCCCAGC	AGGGTGTTTC	CTTGCAGCCT	GGAACCACCC	AGATTTCAC	TCAGACAGAT	240
CCTCTCGAG						249

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTCGGCC	TTCATGGCCT	AGGGATTTTT	TTTCTTTTTT	TTCTCATAT	GTGAAGTAAT	60
AGTCTCTTCA	CAACAGAAGA	AGCCACAAAA	CTAACTTAT	TGGTCACTGA	ATTTTCTTCA	120
AGGTTACGTA	CCTCTTTGGT	ATTTTAAATC	TAGATTATGT	TGATTTTAT	ATTTTGTTC	180
TCATTTTCT	ATTTCTTGT	TTTCTTACT	GCAAATGGGC	TCGAG		225

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

```

GAATTCGGCC TTCATGGCCT AGTTTGGAG AGCTCTACCT ACTAGCTGGT TATTTCTTAC      60
ATTAAATTAA TACCTTTAAA AAGTATTATG AAAATAACAC ACTCAGTAAA AGAAATTTTA      120
AAAAACAAAT GCAATAAAAA TGTGTTTCTT TTCAACCTTT GACTTGTCAC TTCCTCCAGC      180
TTTCCCTTA TTAACTGTG AGAGGTATTC TCTATTAGCA GTTACTTATC CCCTTCCTCA      240
AACTCGAG                                         248

```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

GGATTGAATT CTAGACCTGC CTCGAGCGAC CTCTAGAATC CTACATTGA AATATTCTGG      60
CAGTGAGGTG TTCATCCTAA CTCAGTCAGG TAGCTGTGGA CAGCCTTCAC CTGTTAGGAG      120
CTCCTTAGAA ATAAATTCTG AATACCTTTG GTTTTCTTTT ATCCTCCAGA GGAATTCCA      180
CTATCTCCGA AGCTGTTCTT TGTCCACTG ACAATTCGCT TAGTTAATGT TCTTTTTCAG      240
CCTGTACTAT CTCGAG                                         256

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

GAAGGCAAGA AAATCTATGG AAAGAGAAGG CTACGAGTCC TCGGGCAATG ATGACTACAG      60
GGGTAGTTAC AACACCGTGC TCTCAGGCC TTTATTTGAA AAGCAGGACA GAGAAGGTCC      120
AGCCTCCACG GGAAGCAAAC TCACATTCA GGAACATCTG TACCCCGCGC TTTCATCACC      180
TGAGAAAGAA CAGCTGCTGG ACCGCAGACC CACTGAATGT ATGATGTCGC GATCAGTAGA      240
TCACCTCGAG                                         250

```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

GAATTCGGCC TTCATGGCCT AGCTGGGGGG AATAGGTTAT GTGATAAGGA GTCAGTCGGA      60
CAGAGTGGGG TGAAAGATGT TCAGACAGGG AAACACACAT GCAANAGAGG GAAGGTGGGA      120
CACAGCATAT GCNTCCAACA TTTGGTAGGG CCGAGGCCCC ACATGGGAGC AGTGAGAGGT      180
TAGGGATCGA CGCTCGAG                                         198

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

GAATTTTCCT TACCAGGAAA ATTCATGCTT TACAATTTGT CAGAGGTGCA CATTACTAAT      60
TACAATAGGT CACACTTTTT CTATGCGCTT CATTATAATA TTGGCAACTT TATTATGCCC      120
CATTACATAC TGTATTATGC TCTTACTTTA TATGCATTTT GAG                          163

```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

GAATTGCTGA TATCTTATAA AGGGGACCTT TTTTCTTTAC ATTTCTGACG GTTTTATCA      60
GAATGTATGT ATTAATGCTA TTGTCTTTG TATATTATT TTATTTCCAG CCACTTCTCG      120
AG                                  122

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

GAATTCGGCC TTCATAGCCT AACTCAAGAT CTCCCATCTA TTAAAGCAGA GGAATAACTT      60
TTGTAGGCTT AATACTGCTT TCTCACTTAG GAAAAGTTGA AATTAAGAAC ACACAGGAAG      120
GGATCATTTT CTAAGGTTTA TGTCTCAAC ATCAAATTGA GTTGAAACTT GACTACAGGC      180
CATCTGCTCA TTCAAAGCAT TACAATAAAT CTGTCCTATT GATGATCAAA ATGAGAGCTG      240
AATTGGATGC AGGATTGGAC ATTGCAAGCT GTTCTCCCAA GTGGGATGGA AAGGTGCTCG      300
AG                                  302

```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```
GAATTCGGCC TTCATGGCCT ACAAAAATAT TTATTGACT GAATGATTTA ATATGCAGTT      60
ATGGTGTTTA ATATATCATG TGTTATTTGT TTGTTTAAAT ACAGACATAA CCCACAGTTA      120
TCTTGAACAA GAAACTACGG GGATAAATAA AAGTACGCAG CCAGATGAGC AACTGACTAT      180
GAATTCTGAG AAAAGTATGC ATCGGAAATC CACTGAATTA GTTAATGAAA TAACATGTGA      240
GAACACAGAA TGGCCCGGAC TCGAG                                           265
```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```
GAATTCGGCC TTCATGGCCT ACTTTAATTT CTCTGAGCAG TATTTTACAG TTTTGATGTA      60
TAAACCTGGC ACAGATTATG TTCAGTTTAT TTCTAAGTTT AAGTCATGTT TTTGAATGTT      120
ATATTAAAGG ATATTTTCTT TTTTAAAAAA TCTACAATGT TTATTTTATT ATTATTATTT      180
TTAATCTCGC TTCATCACCA AGGCTGGAGT AAAGTGACGC GACCTCAGCT CGAG           234
```

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

```
GAATTCGGCC TTCATGGCCT ACGCACATCC GCAGTCAGCC ACCTCGGCGC CGCCTCCAGG      60
AGCAAGGATG GAGAGGCTGG TGATCAGGAT GCCCTTCTGT CATCTGTCTA CCTACAGCCT      120
GGTTTGGGTC ATGGCAGCAG TGGTGCTGTG CACAGCACAA GTGCAAGTGG TGACCCAGGA      180
TGAAAGAGAG CAGCTGTACA CACCTGCTTC CTTAAATGTC TCTCTGCAAA ATGCCCAGGA      240
AGCCCTCATT GTGACATGGC AGAAAAAGAA AGCTGTAAGC CCAGAAAACA TGGTCACCTT      300
CAGCGAGAAC CATGGGGTGG TGATCCAGCC TGCCTATAAG GACAAGATAA ACATTACCCA      360
GCTGGGACTC CAAAAC TCAA CCCTCGAG                                           388
```

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

```

GAATTCGGCC TTCATGGCCT AGCTGATATT ATTTCTGAGT TTTTGCTTAT TTGCTTTCTA    60
CATAGAATCA ATAAAATTGA CAACTAGCAT TGCCTATATA TGCAGGTGTG ATACTATTCA    120
GGGTACTAGT ATATTGGCCA CTCATTATGA AACTTTCAGG TCCTCATATA TTTTCTTTTA    180
TTACAATGAT CTAATTATT CTGATAAATA TTGGATTCAT AGAGGCTAAA GGGCTGGGAA    240
AGGAAAACAT TCGTGACTAC TTACAACCAT TTGATACGAG TTGTGTCAAT ACAGACCTCA    300
CACAGCAGCA CCTCGAG                                                    317

```

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```

GAATTCGGCC TTCATGGCCC ACAAATGGT AATACAAATA AACCCTACT TACTGCTTTT    60
AATGGTAGTT TGTTTTTTTT TTTTGAGAC AGAGTCTCGC TGTGTCGCCC AGGCTGGAGT    120
GCAGTGGCGC GATCTTGGCT CACTGCAAGC TCCGCCTTTC GGGTTCACAC CATTTTCTCTG    180
CCTCAGCCTC CCGAGTAGCT GGGACTGCAG GCGCCCGACT CCGGGTTCA CACCATCTC    240
CTCCCTCAGA CTCGAG                                                    256

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

GAATTCGGCC TTCATGGCCT AGGAGAATCG TGAGACCTCT ATTCCATAT CTTTTTCTAC    60
TACTGGAATT TTTATTTTAA CCATACCCAT AAATTACTTT CTATTTTAAG AAGCAAATAT    120
ATAATTCCTC AGTTTAGTAA AAAGTTCTCA CTTGAAAAGC TGGTATATGA ACTTTAGAGG    180
GCAGATTAAT CAACTGCTAA ATATTATTAA TCTTCTTCT TGGAACTTTC CAACACAAAA    240
GACAGTTTAT AGAAAACAAA GTCAGTGTTT AAAACAGCTG AATGAACTAT CTTTGTATAT    300
TTTATTGTGT TTTGTTTGT TTTGTTTGT TGAGACAGAG TCTTGCTCTG TTGTCCAGGC    360
TGGAGAGTAA TGGCAGATG ACTGCAACCT CTGCCTCCCG GGCTCAAGTG ATTCTCCTGC    420
CTCAGTCTCT CGAG                                                    434

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

GAATTCGGCT TCATGGACGA GGAGATCGTG TCCGAGAAGC AAGCCGAGGA GAGCCACCGG    60

```

CAGGACAGCG CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAATC	120
TGGCTCTTCA AGCACCGCCG GGCCCGCTTC CTGCACGAAA CCGGCCTGGC TATGATTTAT	180
GGTCTTTTGG TGGGCCTTGT GCTTCGGTAT GGCATTTCATG TTCCGAGTGA TGTAATAAAT	240
GTGACCCTGA GCTGTGAAGT GCAGTCAAGT CCAACTACCT TACTGGTAAA TGTTAGTGGA	300
AAATTTTATG AGTATATGCT GAAAGGAGAG ATACTCGAG	339

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GAATTCGGCC TTCATGGCCT ACTTATTTT GTTCTGTGT GTTTGTTTAA AATGTGTGTG	60
CGCTCATGTG AGTTTGAAGG GAGTTAGATG CAACAGCAGG AGCTGTGCTC AGGGCAGTGG	120
TGTTAATTAT GGAGGGCGTG GGAAGGGCTG GGAAGAGGAG GGGGTTGTAA GACTCCCTT	180
TTCCCTCGCA TGTAACAGA TGCTGGTGAC TGAAAGTCTG TCTGCGGTAA TTGGCAAGAG	240
TGACGGAAAG CTCGAG	256

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GAATTCGGCC TTCATGGCCT AATTGAAAA TTCATAAGTT TCTACCAATA CTCCCAATT	60
CAATCCAACA TCTGAGGATC TCCCTAGATT TCCTATTTC ATGATTATAA CTCTTGTAAC	120
AGATGATAAG AAACATGGAT CTGACTATAC TCAATTTATT CACATATTTT CTCAGTGAAC	180
TAACTTATTT GCTGAATATA ACCAGTCCCC AGCCTTCCAA CTGCCTCTCT CACTTGCCAC	240
CTCTGCATCT TCCCCACTG TCTCCTCAG CAATCAGACT GCCTCTTGCC AAGTCATCAC	300
CACAGCACCC CACTCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GAATTCGGCC TTCATGGCCT ACCCTCTACT ATTTTGAAC CAAATCAACA ACAACCTATT	60
TAGCTGTTC CCAACCTTTT CCTCGACCC CCTAACAACC CCCCTCCTAA TACTAACTAC	120
CTGACTCCTA CCCCTCACAA TCATGGCAAG CCAACGCCAC TTATCCAGTG AACCACTATC	180
ACGAAAAAAA CTCTACCTCT CTATACTAAT CTCCTACAA ATCTCCTTAA TTATAACATT	240

CACAGCCACA GAACTAATCA TATTTTATAT CTTCTTCGAA ACCACACTTA TCCCCACCCA 300
TCTCGAG 307

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GAATTCGGCC TTCATGGCCT AGTACAATTT AATATAATTT CTTACAAGTT TATTACCTAA 60
AACTTTGCAA ATAATTGAAG TTAGAAGCTT TGGATTGTGT TTTTAGAGCT TAATCCTTTT 120
CTGTAAGTGG AAATCCTTTC CACTGGTTTA TTTTCCTTTT GATTTTATTT TACTTTGACA 180
CCCTAAAGGT TTAGTGTTCC TGTTTTTAAA TCTACTGATC GTTCTTATG AGATTCCTTA 240
GAGTACCCCT CGAG 254

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GAATTCTAGA CCTGCCTCGA GAGGACGCCG GAGAGAAATG AGTAGCAACA AAGAGCAGCG 60
GTCAGCAGTG TTCGTGATCC TCCTTGCCCT CATCACCATC CTCATCCTCT ACAGCTCCAA 120
CAGTGCCAAT GAGGTCTTCC ATTACGGCTC CCGCGGGGC CCTAGCCGCC GACCTGTCAA 180
CCTCAAGAAG TGGAGCATCA CTGACGGCTA TGTCCTCCATT CTCGGCAACA AGGTAGCGCA 240
GCTGCTTTGG GGAGCTCCTC CCTACTGCCC AGCAAACTC GAG 283

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GAATTCGGCC TTCATGGCCT AAAAAGTGGT TCCTATTTTC CTGGTTGAAC CTTGAGTGAT 60
ACACCCAGTA TTGTACCACC CAATTAGTAG ACATTATTTC TTCTTAGGTC ATATTATTCT 120
CAGCTTATAG AGCAAGAAGT TGAAGCTTAA AGGGTTAGAT TACTTGCCCA AGGTAATACA 180
GCAAGAATCT TATTTTCATCC AACCTAGAGT GAATATTTCC CCCACATCTC GAG 233

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 497 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

```
GAATTCGGCC TTCATGGCCT ACTGATGTTG AAGACGACAC CACGGCTTTG ATGGAATATC      60
AGATATTGAA AATGTCTCTC TGCCTGTTCA TCCTTCTGTT TCTCACACCT GGTATTTTAT      120
GCATTTGTCC TCTCCAATGT ATATGCACAG AGAGGCACAG GCATGTGGAC TGTTCAGGCA      180
GAAACTTGTC TACATTACCA TCTGGACTGC AAGAGAATAT TATACATTTA AACCTGTCTT      240
ATAACCACTT TACTGATCTG CATAACCACT TAACCCAATA TACCAATCTG AGGACCCTGG      300
ACATTTCAAA CAACAGGCTT GAAAGCCTGC CTGCTCACTT ACCTCGGTCT CTGTGGAACA      360
TGCTGCTGCT TAACAACAAC ATTAACCTTC TTGACAAATC TGATACTGCT TATCAGTGGA      420
ATCTTAAATA TCTGGATGTT TCTAAGAACA TGCTGGAAAA GGTGTCCTCT ATTAATAATA      480
CACTAAGAAG TCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```
GAATTCGGCC TTCATGGCCT AGCCCCGACT AGCTTTGCCC TAACTCCTTC ATCAAAAGAC      60
CCCCCGCCAG CTTCACACAC CTCATACGCA GCCACATCTG CCCTATTCTC CATGCTTTCC      120
AGCTTGCTCG CCCTTCCTCA TCTCTCCCTG CCTGTGCAGA CCTCCACCCT TCTTTCTCTC      180
ACCCCTCCAT CCCCCAATGC TTGTAGACCT TCCATTCATT CCGTCTCATC GTGCGTGGTC      240
TCTGATCGTC CATCACCTGA CCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```
GTTTACATAA ATATTATACT AGCATTACC ATCTCACTTC TAGGAATACT AGTATATCGC      60
TCACACCTCA TATCCTCCCT ACTATGCCTA GAAGGAATAA TACTATCGCT GTTCATTATA      120
GCTACTCTCA TAACCCTCAA CACCACTCG AG
```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

CAATATTTCA AGCTATACCA AGCATACAAT CAACTCCAAG CTCGGAATTT TAACTTCATG	60
GCAAACAGAA AAGCTAGACT GAGTTATCAG TGTGTGAGA GGAATATTTG GCCCAACAAG	120
AGTTGTTGGG GTGGGAGGAG GGAGAGACAA AAGGAAAGGA CTGCCAGCTC TCAGAGGGTG	180
GAGATGGGGG ACCTCGAG	198

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC TTCATGGCCT ACTGCTATAT TCAAGTTTCT CCCACTACTG TGGTTTCTTT	60
TTTTTTTTTT TTTTTTTTTT TTTTGAGACA GGGTCTTGCT CTGTCACCCA GGCTGGGGTG	120
CAGTGGTGCG ATCTCGGCTC ACTGCAAATT ACACCTCCTG GATTCGAGCA ATTCTCATGC	180
CTCAGCTTCC TGAGTAGCTG GGATAACAGG TATGCACCAC CACCCCTGGC TAATTTTGT	240
GTTTTTAGTA GAGACAAGTT CTCACCATGT TGTCCAAGCC ACCTCGAG	288

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC TTCATGGCCT AAAAGAAGAA TACTAATTAG AATTGAGTT CTAGGGGTTT	60
TTCTAGGTT TTTCATTCTA GACTTAGCTT TTATTCAAAC CTGTTGATCC TGCATAGGGG	120
TAGTCTAGCT TTAATAAATA AAACAATAAA CATAAATGAG CCTATTGAGT TCAATCAGAG	180
TAGGGAGCAG TTTTATTGAA CAGCACATTT TCAAATTCCT CAGTTGTGTT TTGTTTTTCA	240
GCTACGTGTC TCTCTGTGAT AATGAAAAGA CAGGTGCAA AGCCCGGGAA CTAAAATCAG	300
TTTATGTGGA TGCAGTAGGA CTCGAG	326

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

GAATTCGGCC TTCATGGCCT AGTGTAAGT GTTTTGCAC AGTGCCAGA AATTGTCAGT      60
ATTTAATGGT CCTTCCTCCT TATTTATTTT TATTACTTGT TTTTGTITTT TTGAGACAGT      120
GTCTTGCTCT GTCGCCAGG CTGGAGAGCA GTGATATTAT CGTGACTCAC GGCAGCCTCG      180
ACCTCCCAGA CTCAGGTGAT CCCTTCACCT CAGCCTCCCA GGCAGCTGGG ACCATAGCTA      240
TGAACAAACA CGTCCAGCTA TGTTTTGTAT TTTTGTGAA GACGGAGTCT CACCATGTTG      300
CCCAGGCTGA TCTCCAATC CTCGAG                                           326

```

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```

GGAAAGGTGT TGTCCCTTGT AACATTTTGG TTGGCTATAA AGCTGTATAT CGTTTGTGCT      60
TTGGTTTGGC TATGTTCTAT CTCTCTCTCT CTTTACTAAT GATCAAAGTG AAGAGTAGCA      120
GTGATCCTAG AGCTGCAGTG CACAATGGAT TTTGGTTCTT TAAATTGCT GCAGCAATTG      180
CAATTATTAT TGGGGCATTG TTCAATCCAG AAGGAACTTT TACAACTGTG TGGTTTATG      240
TAGGCAACCT CGAG                                                         254

```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

GAATTCGGCC TTCATGGCCT ACAGAAATCT AATCCTGGT GCTATTTGCA ACTACATATA      60
TTTAAAATAC AAGGAGATAA ATACCCAGAA CACATTAAGC CTACTGATTT AAACAGAACA      120
TTTCAAGACT GCTACACAGA AAGGGAAGGA AGCTGTTAAC CCAGCACAGC AGCACACCTC      180
ACATATTTAC GTCTCAGAGA TTAATGGAA AGAAAGGATC AATCAAAACC TTAATGCTC      240
AGTTTTCACA AACACAGTCA AGTCTATCAA ATTTCCAGAT TTACAG                                           286

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

GAATTCGGCC TTCATGGCCT ACAATTAAAA GGTTCTGTTA AATTACGTCT TTCAGTCTGA      60
AATTACTCTG AGAATTTACT TAAAATTTT CCATTTAAAA ACAGGTATAA AATTAATTGC      120
TAGTTTCCAT AATCACCAG TATAAAGATA GAAAAGACCT GTAAGACAAC TGTGTGGTTA      180

```

AATACATGAT AACACATTTA CGTGCCTTTT ATAGAAATCC ACTTATTATG TACATACTGG	240
CTTGTTTTTT TTCCCACTTC TCCAGTACAC TATTTTCAGGC ACAGGCTCAA AATTTGAACC	300
CAAATGGTCT GTTAGGTCTC TTGACTTTTT CAGTTCAAAG CTCTGCTAAT CTGCTAAACC	360
TAGCCCCAAA CCCACTCGAG	380

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GAATTCTAGA CCTGCCCGGA GCCCTGACCT AGTCCGGCGT GGAGAGAGGA ATGGAAAGCA	60
GTGTCCCTTT TGAGAAGGCA AATTACAGC TGGCTTTTGT AATCCTAGCT ATTTTTTGTT	120
TGTTTGCTAA GTCTTTGATA GTCCCCAGTG TGGTTTGCTT GCCAGTGATC TCAGCACCAC	180
CAGAGAGCTT GTTAGAAATG CGGCATCCCA ACCCCACCAC AGCCCTCCCA AGTCAGATAC	240
TCCCCCTCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GAATTCGCTG TGGAGCTGGG CGTGCTGTTC GTCCGGCCCC GGCCCGGAAC CGGGCTGGGT	60
AGAGTGATGC GGACCCTCCT GCTGGTGTCTG TGGCTGGCGA CGCGCGGAAG CGCGCTCTAC	120
TTTCACATCG GAGAGACGGA GAAGAAGTGC TTTATTGAGG AGATCCCGGA CGAGACCATG	180
GTCAATAGGAA ACTACCGGAC GCAGCTGTAT GACAAGCAGC GGGAGGAGTA CCAGCCGGCC	240
ACCCCGGGGC TTGGCATGTT TGTGGAGGTG AAGGACCCAG AGGACAAGGT CATCCTGGCC	300
CGGCAGTATG GTTCCGAGGG CAGGTTCAC TTTANTTCCC ATACCCNTGT GTGAGCACCA	360
GATCTGTTTT CANTCCAATT CCACTCGAG	389

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAATTCGGCC TTCATGGCCT AGAAGGAAAT AAAGGCCCCG ATTTCTGGAG TTCTGAGCCT	60
ACTTTTTTTG GGTGCATTTT GAAACATACG GATTTTACCG CTAGTATATT CAGTGAGGAA	120
GGAAGGCTTC TGAAGGATTG ATGATCCCCA AACTGGATTA TGTGTTTCATG ATAATGGTGT	180
ATTTGGTGGC CTAGCATAGT GAGGTGAGGT AGGTCTTTAA AATGGCTCAT TATAAACATC	240

```

ATTGTTCTG AGCTCACTTG CCCTTGCATC TCCTGCCAGA GTGCTTTGTA CATAGTAGGC      300
CCTCATCAAT GCTTGTAGAT TTAAATTTCG GAGGCACACT TGGAAGACAA TGGTGGCTGG      360
TAAATTAATT ATCAGGGTTA GCAACTTCAT TTCTGCTNAC GCTTAAAAAG TGCTGCGCGA      420
GGAAACTCGA G                                     431

```

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

```

GCCTCTGNTT TTAATTCATT GGCAACTGTT ACGATGGAAG ACCTGATTCG ACCTTGGTTC      60
CCTGAGTTCT CTGAAGCCCG GGCCATCATG CTTTCCAGAG GCCTTGCCTT TGGCTATGGG      120
CTGCTTTGTC TAGGAATGGC CTATATTTC TCCAGATGG GACCTGTGCT GCAGGCAGCA      180
ATCAGCATCT TTGGCATGGT TGGGGGACCG CTGCTGGGAC TCTTCTGCCT TGGAATGTTT      240
TTCCATGTG CTAACCTCC TGGTGTGTT GTGGGCTGT TGGCTGGGCT CGTCATGGCC      300
TTCTGGATTG GCATCGGGAG CATCGTGACC AGCATGGGCT TCAGCATGCC ACCCTCTCCC      360
TCTAATGGGT CCAGCTTCTC CCTGCCCACC AATCTAACCG TTGCCACTGT GACCACACTT      420
CTCGAG                                     426

```

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

```

GAATTCGGCC TTCATGGCCT AAATTTTCAG GCAGTTTGAA GTATCTGGCA GAAAAAGTAA      60
ATTGAAATCA TTGGGACGTT GATTTTTAAA TTACCTAGAA GCAATCCCAA TGCTTTATGT      120
AATACTAAAA TTTCTCCTCT CTCTTTCTT TATCTCTCTC TCCCCTGAAA ATAATCATTT      180
TTTTTCAGT GCCAGTTCAG ATCTTGCAA CAGTTGTTT GAAAAAGTAC CTGAACAAAA      240
TACATTTTAT AAAGTAAAGT ATTCAGGAAC TGACAGAACT GGAGAAGAAT ATATTTATGT      300
TACAGAAGTC ATGGACAACC TCGAG                                     325

```

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

```

GGCAAGTAAC AGGTTGCAAG AATTGGAGGC AGAGCAACAG CAGATCCAAG AAGAAAGAGA      60
ATTACTGTCC AGACAAAAGG AAGCTATGAA AGCAGAGGCA GGCCAGTTG AACAACAATT      120

```

```

ACTACAGGAG ACAGACAAAT TAATGAAGGA AAAACTAGAA GTACAATGTC AAGCTGAAAA    180
AGTACGTGAT GACCTTCAAA AACAAAGTGAA AGCTCTAGAA ATAGATGTGG AAGAACAAGT    240
CAGTAGGTTT ATAGAGCTGG AACAAAGAAA AAATACTGAA CTAATGGATT TAAGACAGCA    300
AAACCAAGCA TTGGAAAAGC AGTTAGAAAA AATGAGAAAA TTTTATAGATG AGCAAGCCAT    360
TGACAGAGAA CATGAGAGAG ATGTATTCCA ACAGGAAATA CTCGAG                      406

```

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

```

GAATTCGGCC AAAGAGGCCT AGTCGGTGCC TCATTGGTAT AAATGTTATG TCTGCATGGG    60
TTTTTCTAC AATTCTTTC TAAGATTATT TCTCCCCAAA GCTCAGCACT TTTGGAATTT    120
TTCATTCTCA TCCAAAAATG GAAGCAATTT TATGTAAATG TCTCTTGGA GCAAGTGTGG    180
AATTCATATT TTGGGTAGCA GAAGCAGTAG TTACAAGGT AGTGGTGTCT TTTGTGGTGG    240
TGGTGGCACC TGCTGCAGTT GTTCATATTT GGGGTGCAGG AGTAGGGAGG GTAGGATCAG    300
TTGAGAATT TACAGGAAA AATGGAGGTC CAGGTGGATA GGTCTAGAA TTCAATC          357

```

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

```

GAATTCGGCC AAAGAGGCCT AAGTGAATCC AGAGCCTCCT GCAAGATGCT GTTGATTCTG    60
CTGTCACTGG CCTTGCTGGC CTGAGCTCA GCTCAGAACT TAAATGAAGA TGTGAGCCAG    120
GAAGAATCTC CCTCCCTAAT AGCAGGAAAT CCACAAGGAG CACCCCCACA AGGAGGCAAC    180
AAACCTCAAG GTCCCCATC TCCTCCAGGA AAGCCACAAG GACCACCCCC ACAAGGAGGC    240
AACCAGCCTC AAGGTCCCCC ACCTCCTCCA GGAACCACAC AAGGACCACC CCCTATTCTC    300
GAG                                                                303

```

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

GAATTCGGCC AAAGAGGCCT AAGCAGACAC AATGGTAAGA ATGGTGCCTG TCCTGCTGTC    60
TCTGCTGCTG CTTCTGGGTC CTGCTGTCCC CCAGGAGAAC CAAGATGGTC GTTACTCTCT    120
GACCTATATC TAACTGGGC TGTCCAAGCA TGTGAAGAC GTCCCGCGT TTCAGGCCCT    180

```

TGGCTCACTC AATGACCTCC AGTTCTTTAG ATACAACAGT AAAGACAGGA AGTCTCAGCC	240
CATGGGACTC TGGAGACAGG TSGAAGGAAT GSAGGATTGG AAGCAGGACA GCCAACTTCA	300
GAAGGCCAGG GAGGACATCT TTATGGAGAC CCTGAAAGAC ATCGTGGAGT ATTACAACGA	360
CAGTAACGGG TCTCACGTAT TGCAGGGAAG GTTTGGTTGT GAGATCGAGA ATAACAGAAG	420
CAGCGGAGCA TTCTGGAAAT ATTACTATGA TGGAAAGGAC AAACCTCGAG	469

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GAATTCGGCC AAAGAGGCCT ACTACTTCTG TAGTCTCATC TTGAGTAAAA GAGAACCCAG	60
CCAACTATGA AGTTCCTTGT CTTGCGCTC ATCTTGGCTC TCATGGTTTC CATGATTGGA	120
GCTGATTCAT CTGAAGAGTA TGGGTATGGC CCTTATCAGC CAGTTCCAGA ACAACCACTA	180
TACCCACAAC CATACCAACC ACAATACCAA CCTGCCTCAA GGTCTCCAC CTCCTCCAGG	240
AAAGCCACAA GGACCACCCC CACAAGGAGG CAACAAACCT CAAGGTCCCC CACCTCCAGG	300
AAAGCCACAA CGACCACCCC CACAAGGAGG CAGCAAGTCC CGAAGTTCTC GATCTCCTCC	360
AGGAAAGCCA CAAGGACCAC CCCACAAGG AGGCAACAAA CCTCAAGGTC CCCACCTCC	420
AGGAAAGCCA CAAGGACCAC CCCACAAGG AGGCAGCAAG TCCCGAAGTG CCCGATCTCC	480
TCCAGGAAAG CCACAAGGAC CATCCACAA CTCGAG	516

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GAATTCGGCC AAAGAGGCCT ACTTCACTTC AGCTTCACTG ACTTCTTGAC TCTCCTCTTG	60
AGTAAAGGA CTCAGCCAAC TATGAAGTTT TTTGTCTTTG CTTAGTCTT GGCTCTCATG	120
ATTTCCATGA TTAGCGCTGA TTCACATGAA AAGAGACATC ATGGGTATAG AAGAAAATTC	180
CATGAAAAGC ATCATTACA TCGAGAATTT CCATTTTATG GGGACTGTGG ATCAAATTAT	240
CTATATGACA ATTGATATCC TTAGTAATCA TGGGGCATGA TTATAGAGGT TTACTGGCA	300
AATTCACTTT TACTCATTTA TTCTCATTCA TCACACCGCA AGTCTAGGCC TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```

GGTTACCATC CTCAAAGGAT TGGCTAAAAG CAAGCAACTG GATTGAACAC CCTAAGAAGA      60
AAGATTCACA CTGCACCAGG AGACATCAGA AAGAATGAAA ACTCTGCCGC TGTTTGTGTG      120
CATCTGTGCA CTGAGTGTCT GCTTCTCGTT CAGTGAAGGT CGAGAAAGGG ATCATGAACT      180
ACGTCACAGG AAGGCATCAT CACCAATCAC CCAAATCTCA CTTTGAATTA CCACATTATC      240
CTGGACTGCT AGCTCACCAG AAGCCGTTC TTAGAAAAGTC CTATAAATGT CTGCACAAAC      300
GCTGTTAGGC CTAAGCTTCC ACCTTCACCT AATAACCCCC CCAAATTTCC AAATCCTCAC      360
CAGCCACCTA AACATCCAGA TAAAAATAGC AGTGTGGTCA ACCCTACCTT AGTGGGTACA      420
ACCCAAATTC CATCTGTGAC TTCCCATCA GCTTCCACCA AAATTACTAC CCTTCCAAAT      480
GTGACTTTTC TTCCCCAGAA TGCCACCACC ATATCTTCAA GAGAAAATGT TAACACAAGC      540
TCTTCTGTAG CTACATTAGC ACCCAGTGAA TTCCCCAGCT CCACAAGACA CCACAGCTGC      600
CCCACCCACA CCTTCTGCAA CTACACCAGC TCCACCCCTC GAG                        643

```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

GAATTCGGCC AAAGAGGCCT ACAAGATGCT GCTGGTCCTG CTCTCAGTGG TCCTTCTGGC      60
TCTGAGCTCA GCTCAGAGCA CAGATAATGA TGTGAACAT GAAGACTTTA CTTTCACCAT      120
ACCAGATGTA GAGGACTCAA GTGAGAGACC AGATCAGGGA CCCAGAGAC CTCCTCCTGA      180
AGGACTCCTA CCTAGACCCC CTGGTGATAG TGGTAACCAA GATGATGGTC CTCAGCAGAG      240
ACCACCAAAA CCAGGAGGCC ATCACCGCCA TCCTCCCCCA CCTCCTTTTC AAAATCAGCA      300
ACGACCACCC CAACGAGGAC ACCGTTTCAT TCGAG                        335

```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

GAATTCGGCC AAAGAGGCCT AGACACATTG CCTTCTGTTT TCTCCAGCAT GCGCTTGCTC      60
CAGCTCCTGT TCAGGGCCAG CCCTGCCACC CTGCTCCTGG TTCTCTGCCT GCAGTTGGGG      120
GCCAACAAAG CTCAGGACAA CACTCGGAAG ATCATAATAA AGAATTTTGA CATTCCCAAG      180
TCAGTACGTC CAAATGACGA AGTCACTGCA GTGCTTGCAG TTCAAACAGA ATTGAAAGAA      240
TGCATGGTGG TTAAAACTTA CCTCATTAGC AGCATCCCTT CTACAAGGTG CATTAACTA      300
TAAGTATAAC TGCCAACCTC GAG                        323

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GAATTCGGCC AAAGAGGCCT AGTGACACCA GAGCCTCCTG CAAGATGCTT CTGATTCTGC	60
TGTCAGTGGC CCTGCTGGCC TTCAGCTCAG CTCAGGATTT AAATGAAGAT GTCAGCCAGG	120
AAGATGTT	128

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GAATTCGGCC AAAGAGGCCT AATTTTGACC AGCAGATTAA TCAACTGTAA GACGGATCCT	60
CACACAAAGA GGCAACTGAA AGGATGAAAT CACTGACTTG GATCTTGGGC CTTTGGGCTC	120
TTGCAGCGTG TTTCACACCT GGTGAGAGTC AAAGAGGCCC CAGGGGACCA TATCCACCTG	180
GACCGCTGGC TCCTCCTCAA CCTTTTGGCC CAGGATTTGT TCCACCACCT CCTCCTCCAC	240
CCTATGGTCC AGGGAGAATC CCACCTCCTC CTCTGCAGAG AAAACCTTTG AAGAAAAGCA	300
GGAACAGAGA TCGATGGCGA TCTATTTCCT TGTACTATAC TGGAGAGAAA GGTCAAAATC	360
GTCTGAG	366

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GGTTTCCCGT TTGTCCCTCC TTCAAGGTTT TTTTCAGCAG CTGCAGCACC CGCTGCCCCA	60
CCTATTCAGC CTGAGCCTGC TGCAGCTGCA CCTCTTACAG CCACACCTGT AGCAGCTGAG	120
CCTGCTGCAG GGGCCCCTGT TGCAGCTGAG CCTCCTGCAG AGGCACCTGT TGGAGCTGAG	180
CCTGCTGCAG AGGCACCTGT TGCAGCTGAG CCTGCTGCAG AGGCACCTGT TGGAGTGGAG	240
CCAGCTGCAG AGGAACCTTC ACCAGCTGAG CCTGCTACAG CCAAGCCTAG GCCTCT	296

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CTCAGATCCT TGTGGCTTTC CTGGAGGTGG GGGACCTTGA GGTTTGTTGC CTCCTTGTGG	60
GGGTGGTCCT TGTGGCTTTC CTGGAGGAGG TGAAGGACCT TGAGGCTGGT TGCCTCCTTG	120

TGGGGGTGGT	CCTTGTGGCT	TTCCTGGAGG	AGATCGGGGA	CTTCGGGGAC	TTGTCTCCTT	180
GTGGGGGTGG	TCCTTGTGGC	TTTCCTGGAG	GTGGGGGACC	TTGAGGTTTG	TTGCCTCCTT	240
GTGGGGGTGG	TCCTTGTGGC	TTTCCTGGAG	GAGGTGGGGG	ACCTTGAGGC	TGTTTGCCTC	300
CTTGTGGGGG	TGGTCCTTGT	GGCTTTCCTC	GAGGAGATGG	GGGACCTTGA	GGTTTGTGTC	360
CTCCTTGTGG	GGTGCTCCT	TGTGATTTC	CTGCTATTAG	GGAGGGAGAT	TCTTCCTGGC	420
TGACATCTTC	ATTTAAGTTC	TGAGCTGAGC	TCAGGGCCAG	CAGGGCCACT	GACAGCAGAA	480
TCAACAGCAT	CTTGCAAGAG	GCTCTGGAGT	CACCTAGGCC	TCTTTGGCCG	AATTC	535

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GAATTCGGCC	AAAGAGGCCT	AGTCGGTAAT	CACAACAAAC	ACGGAGCAAT	CTCAATGCTG	60
TTTATCGGA	GGACAGTCTG	CGGGGTCGTG	ACGATTCTTT	TCTTCTTGAA	GTTTTTCCTT	120
TTCTGAATC	TCATAATGAT	TCTTGCCCAT	GATTCTGTCT	TTCAATGAC	TGTGGCTTCT	180
ACTCGAACA	GATCCTTTCC	GAGGAGTGGC	TTGCCAAGCA	GCGTGAAGTT	GTCTGCCCCA	240
ACCAGCAGGA	CCTTCTCCAG	TGCAATTCTC	TCTCCACACG	CAAGGTCTAG	TTCATTTCGA	300
ATTAAGATCA	GGTCTTCAGA	G				321

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GAATTCGGCC	AAAGAGGCCT	AACCTGCCTT	GGTCTTGCT	CCTCTTTCCA	CGTTGGATAA	60
CAATTTTITG	GTTGTTTGT	TTAAGTTGGT	GCTCTGAAGC	TTAATCTCAG	TACCCCTTAC	120
TCTGAATTGT	CAAATTTTGA	TAAACGTGC	CATTTTCTTT	GGTAAGAGAA	AGCAGGTCTT	180
AATGTCTGCC	AGAACAAT	TTATATGCCT	TATTGGCTTC	ATTAAACTTT	TAGAAACTT	240
TAGCATTTGT	TACTTTTTC	CATTGCATTT	ACTTTCAAAT	GCACCTAATG	AATTCGTCAC	300
CCAGTCGCAA	CTTTTCCTT	CTCTGTCCA	TTGCTTTCTC	CTTTCCCCAA	CGCAGCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

```

GAATTCGGCC AAAGAGGCCT AAAGCGACCA AGATAAAAGT GGACAGAAGA ATAAGCGAGA      60
CTTTTATCC ATGAAACAGT CTCCTGCCCT CGCTCCGGAA GAGCGCTACC GCAAAGCCGG      120
GTCCCCAAG CCGGTCTGA GAGCTGATGA CAATAACATG GGCAATGGCT GCTCTCAGAA      180
GCTGGCGACT GCTAACCTCC TCCGGTCCCT ATTGCTGGTC CTGATTCCAT GTATCTGTGC      240
TCTCGTTCTC TTGCTGGTGA TCCTGCTTTC CTATGTTGGA ACATTACAAA AGGTCTATTT      300
TAAATCAAAT GGGAGTGAAC CTTTGGTCAC TGATGGTGAA ATCCAAGGGT CCGATGTTAT      360
TCTTACAAAT ACAATTATA ACCAGAGCAC TGTGGTGTCT ACTGCACATC CCGACCAACT      420
AGGCCTCTTT GGCCG                                     435

```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```

GAATTCGGCC AAAGAGGCCT AGAAATATAT TTTCTAGTGA ATTCTTATTG GAAGCCAGGT      60
CTCTCCTCTC ATTAGATCAA AAGGGACTTA TGTACATACA ACAATTGAAA GTGTTACTCG      120
AG                                     122

```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```

GAATTCGGCC AAAGAGGCCT AAGAAAATCA GCCTGTCTGC TCTCTCCTTG GCTCAACAAG      60
GCCTCTAACA GTCTTCTGTC CTCTATTCTG CACACGGCAT ATTTGGGAAC GAGAAACAAA      120
AGTTTTCCCA AATGAAGAGA ACTCACTTGT TTATTGTGGG GATTTATTTT CTGTCCTCTT      180
GCAGGGCAGA AGAGGGGCTT AATTCCCCA CATATGATGG GAAGGACCGA GTGGTAAGTC      240
TTTCCGAGAA GACCCTCGAG                                     260

```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```

GAAAGAGGCC TACCAACATG CCAGAGGCCG TACCCATATC CGCAGCAG      48

```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```

GAATTCGGCC TTCATGGCCT ACCCTGTCAA AATTTTGCCT CCTCTTGATT TTCAATATAT      60
ATATATTTTT TTGTCTTACT CTGTTGCCCA GGCTAGAGTG CAGTGACGTG ACCTTGGCTC      120
ACTGCAACCT CTGCCTCCTG GGCTCAAGCA ATCCTCCCAC CTCAGCCTCC TCAGTAGCTG      180
GGACCACAGG CATATGCTAC AAAGCCCAGA TTATTTTTTT ATAGAAACAG GGTTCACCA      240
TGTTGCCCAG GCTTGTCTCG AACCCAGAA CTCGAG      276

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

GAATTCGGCC TTCATGGCCT ACAAATGCCC ATCAAAGACT GGATAAGAA AATGTAGTAT      60
ATATATATAT ACCATGGAAT ACTGTGCAGC CATAAAAAAG GAATGAGATC ATGTGTTTCA      120
CAGGGATGTG GATGAAGCTG GAAGCCATCA TCCCAGCAG ACTAACACAG GAACAGAAAA      180
CCAAACACTG CATGTTCTCA CTCATAAGTG GGAGCTGAAC AATGAGAACA GGTGGGCACA      240
GGGACGGGAA CAACACACAC CAGGCGCTGT TGTGTGGTGG GGGTGAGGGT TGGAACTCGA      300
G      301

```

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

GCGAGGCAGG GAAACTCACT TCACGTCTCT TTCCTTGTAG AGCATCATGC TTATTTCTGG      60
CTCACTCACA TCTTTGTCTC GGGAGTTCTC TGCCGAGCCA TTGCCCCCTA CAGCAGAGAG      120
CACAGCTGGC TGCACTAGTG CTGAAGGAGC CAGCCCCAGA GCAGGGCATT TCCAGGGGCT      180
CTTGTCCTCAG AGCGGCAGGC GTTGTGTGCA GAGAACGCCC CTCCCACGCA GCACAGAGAA      240
CGCGGGGTGG GTGTGTGGCT CCGGGCCTGT GGGGCTTAGG CTGCCTGAAC CACCGCCGAC      300
TGGCACCATG ACTCGGCATT CCTGGAAGTG CCTTACCAAG TTGTTGTTGT TGTTTTGTG      360
TTTTTTAAGA GACGGGCTTG CTCTATCATC CAGGCTCGAG      400

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GAGATAAACA AAATTGATTG CCCCATTTCTC TCACTTCCCC ATCTTGTCTT CCTAGACCCC	60
ACAGAGTTAA AACTTGGGAT TCCCCTGGCC CCCCAGAAC ACTTGTATAT TGTTTGTTTG	120
AGGTTCGTGC CGCAGTAACA GACACAGTAT TTAATTGCAC ATACAGATGT TTGCTGGGTA	180
TATTCAGTGT AAATTTTATT TAATCTGTTT TTTTGTGTTT TTGGGGGTTA TTTGGGGGGA	240
GGTTGGTTTT GTTTTAAAT ATAAAAAAA AAATCTGTCA CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GGCCTCACCT TACCCAGGA CTCCGCTATG ACACCGCCTC TGCCCTACA AGACACAGAT	60
CTCTCGTCAG CCTCAAAGCC TGTGGCTGCA GCCACGCCTG TGTCCAGCA GGCTGAAGAG	120
GGCCTCACCT TACCCAGGA CTCCGCTATG ACACGACCTC TGCCTCTGCA AGACACAGGC	180
CCCACCTCAG GTCCAGAGCC TCTGGCTGTG GCCACCCCTC AAACCTTGCA GGCAGAAGCA	240
GGCTGTGCCC CAGGGACAGA GCCTGTGGCC ATACTCGAG	279

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GCAATGGCAG GAATTCGAAA TATTGGCATA TGTTCTTTT GGATTAGATT ATATAAATC	60
AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTCTCT GCATGATACT TCTGCTTATT	120
GTCCTTCACA CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC	180
CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT	240
TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```
GAATTCGGCC TTCATGGCCT AAGGAGAATG GCGTGCACCC GGGAGGCGGA GCTTGCAGTG      60
AGCCAACATC ACGCCACTGC ACTCCAGCCC GGGCGACTGA GCGAGACTCT CTCTCNAAAA      120
AAAAAAAAAA AAAGAAAAAG AAAAAGAAAA AGAAAAAGAA AAGAAAATAT ATANATACAC      180
ACAGAGACTG AGAGAGAGAG AGAGAGAGAG ACCAGAAAAA GAGAGAAGGA GAAAGAGAGA      240
ATGCAAAAAC CAAGAGGANA GAATGATCCA CTCTCCAAC T AGAAAGGTAG CTCTCAATCT      300
GAAAAGTCAC TTGATTACTT TGTCTATTTT GCTTATCTGC TACATCAATG GTTCCCTCGA      360
G
```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

```
GAATTCGGCC TTCATGGCCT AGGCCTTTTC TTTTAAAGG AATTCAAGCA GGATACGTTT      60
TTCTGTTGGG CATTGACTAG ATTGTTGCA AAAGTTTCGC ATCAAAAACA ACAACAACAA      120
AAAACCAAAC AACTCTCCTT GATCTATACT TTGAGAATTG TTGATTTCTT TTTTATTTC      180
TGACTTTTAA AAACAACCTT TTTTCCACT TTTTAAAAA ATGCACTACT GTGTGCTGAG      240
CGCTTTTCTG ATCCTGCATC TGGTCACGGT CGCGCTCAGC CTGTCTACCC GCAGCACACT      300
CGAG
```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

```
GGGGCTGCGG GGATTGACCT CCTCACTTCT GGGTTGCCAC TCGAAGCTTG CTCCGGGCAA      60
CGACCCTGCT GCTTCCCAGA GGGAAACTGT AGCCCCACAGA CCAGGAGAGA AGCCAAAGCA      120
CCTGCTCCAC GTCCACATCA CCCCAGGCTT CTAGCCCCCA GGGGCTTCAT CAGTGCTTCA      180
GCGCTCTCTC CCATCCCCCA CTCCCATGT CCCTCGTGAT CCGAACTCCT AGGGCTCCGT      240
GTCCACAGG TCACCACTTC CGGCTGTCTC GAG
```

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

GAATTCGGCC TTCATGGCCT ACATCAATAA AATACATTCT ACACAGAATA CGCCAACCAT      60
ACACTACTCT TTTTIGATAA TAAAAAATGT ATTTACTGAG CCAGTTGTGG TGGCTCGCGC      120
CTATAATCCC AGCACCTTGG AAGGCCAATG GGAGTGGATC GGTGAGGCC AGGAGTTTGA      180
GACCGGCCTG GCCAACATGG TGGAATGCCG TCTCTACTGA GAATGCAGAA ATGAGCCGGG      240
CACGGTGGCA CGCACCTGTA GTCCCAGGTA CTCGATTCC TCTCGAG                      287

```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

```

AAGAGGCGAT GCGGGCGATG GCATCTCTCG GCGCCCTGGC GCTGCTCCTG CTGTCCAGCC      60
TCTCCGCTG CTCAGCCGAG GCCTGCCTGG AGCCCCAGAT CCCCCCTCC TACTACACCA      120
CTTCTGACGC TGTCAATTC ACTGAGACCG TCTTCATTGT GGAGATCTCC CTGACATGCA      180
AGAACAGGTT CCAGAACATG GCTCTCTATG CTGACGTCGG TGGAAAACAA TTCCCTTGTC      240
CACTCGAG                      248

```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

```

GGCGATGATT AGGCCAGACC CTCCCATCC TCGTGAGGGC CAGAAGCTGT TGCTACACTG      60
TGAGGGTCGC GGCAATCCAG TCCCCAGCA GTACCTATGG GAGAAGGAGG GCAGTGTGCC      120
ACCCCTGAAG ATGACCCAGG AGAGTGCCCT GATCTCCCT TTCCTCAACA AGAGTGACAG      180
TGGCACCTAC GGCTGCACAG CCACCAGCAA CATGGGCAGC TACAAGGCCT ACTACACCCT      240
CAATGTTAAT GACCCAGTC CGGTGCCCTC CTCCTCCAGC ACCTACCAG CCATCATCGG      300
TGGGATCGTG GCTTTCATTG TCTTCCTGCT GCTCATCATG CTCATCTTCC TCGGCCACTA      360
CTTGATCCGG CACAAAGGAA CCTACCCTAC ACTCGAG                      397

```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```

GUCTGCCTCC AGGCCTTTGC TCCCACTGTT GCCTCCACTT AGAATAACAT TCCACCCCAT      60
CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCTTA AGGCCAGTTC TAACCCTAAC      120
TGACAACAAA TCATCTCTAC ATGATCTTTT CTTCTGGGA ATGCCTGCAG CACTGTTTAA      180
TCCTGCCCCA CCACCATCCC CTCACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA      240
TGCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

GAATTCGGCC TTCATGGCCT ACTATGCCGT CATGATAGAG AAGATGATCC TGAGAGACCT      60
GTGCGGTTTC ATGTTTGTCT ACGTCGTCTT CTTGTTGGG TTTCCACAG CGGTGGTGAC      120
GCTGATTGAA GACGGGAAGA ATGACTCCCT GCCGTCTGAG TCCACGTCGC ACAGGTGGCG      180
GGGGCCTGCC TGCAGGCCCC CCGATAGCTC CTACAACAGC CTGTACTCCA CCTGCCTGGA      240
GCTGTTCAAG TTCACCATCG GCATGGGCGA CCTGGAGTTC ACTGAGAACC ATGAACTTCT      300
CGAG      304

```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

```

GAATTCGGCC TTCATGGCCT AGGAACCTGG ACCGCGGCGG CGCGGGTTT CCCTCATGAT      60
CCCGGCGGG CGGCGGCGGC GGCAGAGGCG GCGGGAGGAT GACCTCTTAC CGGGAGCGGA      120
GTGCCGACCT GGCCCGTTTC TACACTGTCA CCGAGCCCCA GCGACACCCG AGGGGCTACA      180
CAGTATATAA GGTCAACGCC CGGGTTGTTT CACGAAGAAA TCCAGAGGAT GTCCAGGAGG      240
GAGAATCCTG AACCAACCTA TCCATGAACA TACTCTCTGC CATTTTCTTA GTCCTTTCTT      300
CGGAAAAACT CGAG      314

```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```

GAATTCGGCC TTCATGGCCT ACCAACTTAA GAAAATGAGA CTGAGCAATC TCATGGTTCT      60
TGGACAGTTA GTCTATGGCC AATTGATGGA ACCAGTAAAT CGAGAGAACT TTACGCAGAC      120
CTTGCCCAAA ATGCCAATTC ATTCTCATGC ACAGCCCCCA GATGCCAGGG AAGAGGATAT      180

```

CATACTTGAA	GGTCAACAGA	GCCTGCCATC	CCAGGCTTCA	GATTGGAGCC	GATACTCAAG	240
CAGCTTACTG	GAATCCGTCT	CTGTTCTGG	AACACTAAAT	GAGGCTGTTG	TAATGACTCC	300
ATTTTCATCG	GAACCTCAAG	GAATTTGAGA	ACAGACCCTC	CTGGAGCTGT	CCAAAGGAAA	360
GCCCTCCCCG	CATCCCAGAG	CCTGGTTTGT	GTCTCTTGAT	GGAAAGCCAG	TTGCACAAGT	420
GAGGCACTCC	TTTATAGACC	TGAAAAAGGG	CAAGAGAACC	CAGAGCAATG	ACACCAGTCT	480
GGACTCTGGG	GTGGACATGA	ATGAGCTTCA	CTCAAGTAGA	AAGCTCGAG		529

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GGAGATGAAA	GTAAAGTG	AAAACCTTAA	AGAGGAGCCT	CAGTCTTCTG	AAGAAGAATC	60
TATGTCTTCT	GTGAAACCA	GGACACTAAT	AAAATCTGAG	CCTGTAAGTC	CAAAGAATGG	120
TGTTTTACCA	CAGGCTACTG	GAGACCAGAA	ATCTGGTGGA	AAATGTGAAA	CAGACAGACG	180
CATGTTGCA	GCCAGAACAG	AACCCCTAAC	TCCAAACCCA	GCTTCTAAGA	AACCAAGAGT	240
CCACAAAAGG	GGATCAGAAT	CTAGTTCTGA	TTCTGACTCA	GATTCTGAGA	GATCATCTTG	300
TTCTTCCAGA	TCATCTTCTT	CCTCATCATC	CTCTTCTTGT	CCCACTCTCG	AG	352

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GTCTACACCN	TTCCGAGTTG	GCTGCAGATT	TGTGGTGCCT	TCTGAGCCGT	CTGTCCTGCG	60
CCAAGATGCT	TCAAAGTATT	ATTAAAAACA	TATGGATCCC	CATGAAGCCC	TACTACACCA	120
AAGTTTACCA	GGAGATTTGG	ATAGGAATGG	GGCTGATGGG	CTTCATCGTT	TATAAAATCC	180
GGGCTGCTGA	TAAAAGAAGT	AAGGCTTTGA	AAGCTTCAGC	GCCTGCTCCT	GGTCATCACT	240
AACCAGATTT	ACTTGGAGTA	CATGTGAAAG	AAAACGTCAG	TCTGCCTGTA	AATTTAGCA	300
AGCCGTGTTA	GATGGGGAGC	GTGGAACGTC	ACTGTACACT	TGTATAAGTA	CCGTTTACTT	360
CATGGCATGA	ATAAATGGAT	CTGTGAGATG	CACGTGCTACC	TGGTACTGCT	TTCAGTGTGT	420
TCCCCCTCAG	CCCCTCCGGC	GTGTCAGGCA	TACTCTGAGT	AGATAATTTG	TCATGCAGCG	480
CATGCAATCA	GAATCTCGAG					500

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

```

GAATTCGGCC TTCATGGCCT AGATGCTCAA CACCTCCTCC TTGGTGGAGC AGCTGAACGA      60
GCAGTTTAAC TGGGTGTCCC GGCTGGCAAA CCTCACGCAA GCGGAACACC AGTACTATCT      120
GCGGGTCACC ACGGTGGCTT CCCACACTTC TGA CTGGAC GTTCCTTCCG GTGTCACTGA      180
GGTGGTCGTG AAGCTCTTTG ACTCTGATCC CATCACTGTG ACGGTCCCTG TAGAAGTCTC      240
CAGGAAGAAC CCTAAATTTA TGGAGACCGT GGCGGAGAAA GCNCTGCAGG AATACCGCAA      300
AAAGCACCGG GAGGAGTGAG ATGTGGATGT TGCTTTTGCA CCTACGGGGG CATCTGAGTC      360
CAGCTCCCCC CAAGATGAGC TGCAGCCCCC CAGAGAGAGC TCTGCACGTC ACCAAGTAAC      420
TCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

```

GAATTCGGCC TTCATGGCCT AATCTTAAGG GACCTTTCCT TACTACAGAT TCAAATGCGA      60
GATCTTGAGG GTTACAGGGA AACGAGGTAT CAGTTACTTC AGCTTCGACC TGCGCAGAGA      120
GCATCATGGA TTGGTTATGC TATTGCTTAC CATTTATTAG AAGATTATGA AATGGCAGCA      180
AAGATTTTAG AAGAATTTAG GAAAACACAA CAGACATCCC CTGACAAGGT GGATTATGAA      240
TATAGTGAAC TACTCTTATA TCAGAATCAA GTTCTTCGGG AAGCAGGTCT CTATAGAGAA      300
GCTTTGGAAC ATCTTTGTAC CTATGAAAAG CAGATTTGTG ATAAACTTGC TGTAGAAGAA      360
ACCAAAGGGG AACTTCTGTT GCAACTATGT CGTTTGAA

```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```

GAATTCGGCC TTCATGGCCT ACTTATCTTA ATCCAATGGG TGACATCTTC AACAAACCCTG      60
TTCCAAATAA GGCTGCATTC TAAACACTAG GGATTAAGAC ATCAACATGT GAATTTTGGA      120
GGAATGTAGT TCTAACCATA ACAGCAGTGA ATGAGATGAC AGACTATTGC TCTCAAAGA      180
TAGCCAGGTT TCTAGTTTCC TTAGGCATTT TCTGGAGGTT TGCGAGCAGT TCATTATTAT      240
CTTAAAAATA TTATCCAGAG CTGTGGTCTA TCAGCAGCTC ATTACCAGAC TGGCAGATAC      300
ATTTAATCAG CAAAAGAGTT GTTCTGTGTA TTAGCATCCT CCTGGTTTCC CAGCTCAAGA      360
GTTCTTCTGA GTAATAGTAA TCCTTCCCCC ATGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GCTGAAGTGG	TGACTTTTGA	GAGAGGACAC	AAAATTATCA	TCAGCTCCAG	TCGGAGAATC	60
CAGAAAGGAG	AAGAGGTAAG	AGTGTGAGAG	ATTGCATCTG	CCATGTTGTT	CAGATCCTGG	120
GCGAATAGTT	CCCTCCTCAC	ACAGGTCACT	TACTCACTTG	TTTCCCAATT	CTTGTTGTG	180
ATAAAACTC	TGTCCATAAT	AGGCCAGATG	TTCCCACCCT	GCAGTATCTC	ACCCTTCAGG	240
CACTCCAGTT	CACCTTCCTC	CACATCCCTC	GAG			273

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GCTTTAAGAA	TTAACGAAAG	CAGTGTCAAG	ACAGTAAGGA	TTCAAACCAT	TTGCCAAAAA	60
TGAGTCTAAG	TGCATTTACT	CTCTTCCTGG	CATTGATTGG	TGGTACCACT	GGCCACTACT	120
ATGATTATGA	TTTTCCCTA	TCAATTTATG	GGCAATCATC	ACCAAATGT	GCACCAAGAT	180
GTAAGTCCCC	TGAAAGCTAC	CCAAGTGCCA	TGTACTGTGA	TGAGCTGAAA	TTGAAAAGTG	240
TACCAATGGT	GCCTCCTGGA	ATCAAGTATC	TTTACCTTAG	GAATAACCAG	ATTGACCATA	300
TTGATGAAAA	GGCCGCACTC	GAG				323

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GGAAAAGAA	GAGAAAGCCA	AGGAAGACAA	GGGCAAACAA	AAGTTGAGGC	AGCTTCACAC	60
ACACAGATAC	GGAGAACCAG	AAGTGCCAGA	GTCAGCATTC	TGGAAGAAAA	TCATAGCATA	120
TCAACAGAAA	CTTCTAAACT	ATTTTGCTCG	CAACTTTTAC	AACATGAGAA	TGTTAGCCTT	180
ATTTGTGCGA	TTTGCTATCA	ATTTTCATCTT	GCTCTTTTAT	AAGGTCTCCA	CTTCTTCTGT	240
GGTTGAAGGA	AAGGAGCTCC	CCACGAGGCT	CGAG			274

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

GCCCCAGTCC	AGATCCAGGA	CTGAGATCCC	AGAACCATGA	ACCTGGCCAT	CAGCATCGCT	60
CTCCTGCTAA	CAGTCTTGCA	GGTCTCCCGA	GGGCAGAAGG	TGACCAGCCT	AACGCGCTGC	120
CTAGTGGACC	AGAGCCTTCG	TCTGGACTGC	CGCCATGAGA	ATACCAGCAG	TTCACCCATC	180

CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG TGCTCTTTGG CACTGTGGGG 240
GTGCCTGAGC ACACATACCG CTCCCTCCTC GAG 273

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GAATTCGGCC TTCATGGCCT ACTCTCCTAT AAAGCAGACG CCGCGCCGCG CTGCGACGCT 60
GTAGTGGCTT CGTCTTCGGT TTTTCTCTTC CTTCGCTAAC GCCTCCCGGC TCTCGTCAGC 120
CTCCCGCCGG CCGTCTCCTT AACACCGAAC ACCATGCCTT CAATTAAGTT GCAGAGTTCT 180
GATGGAGAGA TATTTGAAGT TGATGTGGAA ATTGCCAAAC AATCTGTGAC TATTAAGACC 240
ATGTGGAAG ATTGGGAAT GGATGATGAA GGAGATGATG ACCCAGTTCC TATACCAAAT 300
GTGAATGCAG CAATATTTAA AAAGGTCATT CAGTGGTGCA CCCACCACAA GGATGACCCT 360
CCTCCTCCTG AAGATGATGA GAACAAAGAA AAGCGAACAG ATGATATCCC TGTTTGGGAC 420
CAAGAATTCC TGAAAGTTGA CTAAGGAACA CTCGAG 456

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GAATTCGGCC TTCATGGCCT AATGGGACAA CTCCTCGCCC TCTACCTGTC CCCTCCCCCT 60
TTGGTTGTAT GATTTTCTTC TTTTTTAAGA ACCCTGGAA GCAGCGCCTC CTTCAGGGTT 120
GGCTGGGAGC TCGGCCCATC CACCTCTTGG GGTACCTGCC TCTCTCTCTC CTGTGGTGTC 180
CCTTCCCTCT CCCATGTGCT CCGTGTTTCTG TGGTGATATAT TTCTTCTCCC AGACATGGGG 240
CACACGCCCC AAGGGACATG ATCCTCTCCT TAGTCTTAGC TCATGGGGCT CTTTATAAGG 300
AGTTGGGGGG TAGAGGCAGG AAATGGGAAC CGAGCTGAAG CAGAGGCTGA GTTAGGGGGC 360
TAGAGGACAG TGCTCCTGGC CACCCAGCCT CTGCTGAGAA CCATTCCTGG GATTAGAGCT 420
GCCTTTCCCA GGGAAAAAGT GTCCGACTCG AG 452

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GCGATTGAAT TCTAGACCAG ACTCGTCTCA GGCCAGTTGC AGCCTTCTCA GCCAAACGCC 60
GACCAAGGAA AACTCACTAC CATGAGAATT GCAGTGATT GCTTTTGCCT CCTAGGCATC 120

ACCTGTGCCA TACCAGTTAA ACAGGCTGAT TCTGGAAGTT CTGAGGAAAA GCAGCTTTAC	180
AACAAATACC CAGATGCTGT GGCCACATGG CTA AACCCCTG ACCCATCTCA GAAGCAGAAT	240
CTCCTAGCCC CACAGACCTT TCCAAGTAAG TCCAACGAAA GCCATGACCA CATGGATGAT	300
ATGGATGATG AAGATGATGA TGACCATGTG GACAGCCAGG ACTCCATTGA CTCGAATCGA	360
CTCGAG	366

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GCCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA ACCTGGCCAT CAGCATCGCT	60
CTCTTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCAGCCT AACGGCCTGC	120
CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG TTCACCCATC	180
CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG TGCTCTTTGG CACTGTGGGG	240
GTGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA GCAAATACAA CATGAAGGTC	300
CTCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT ACACGTGTGC ACTCCACCAC	360
TCTGGCCATT CCCCACCCAT CTCTCCCGA AACGTTACAG TGCTCGAG	408

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GTAGGTCACA GCAGAAGCAG CCAAAATGGA TCCCCAGTGC ACTATGGGAC TGAGTAACAT	60
TCTCTTTGTG ATGGCCTTCC TGCTCTCTGG TGCTGCTCCT CTGAAGATTC AAGCTTATTT	120
CAATGAGACT GCAGACCTGC CATGCCAATT TGCAAACCTC CAAAACCAAA GCCTGAGTGA	180
GCTAGTAGTA TTTTGGCAGG ACCAGGAAAA CTGTGTTCTG AATGAGGTAT ACTTAGGCAA	240
AGAGAAATTT GACAGTGTTT ATTCCAAGTA TATGGGCCGC ACAAGTTTGT ATTCGGACAG	300
TTGGACCCCTG AGACTTCACA ATCTTCAGAT CAAGGACAAG GGCTTGATC AATGTATCAT	360
CCATCACAAA AAGCCACAG GAATGATTCT CATCCACCTC GAG	403

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAATTCCTCT TCTTTACCCT CGTCCTGCCG GGCACCTTCC TTAGGTTTGG TTTCATCTAC	60
-------------------------------------------------------------------	----

AGCTTCTATG	TTCTCTTCAG	CTTGGCTGCT	CTCCCCAGTC	TCCGTTGGAG	GCTGGGCTGT	120
TGCCTTGGCA	GCAGCATCCT	CTGCGGCAGG	GGTGGTGGCA	GCAGCAGCAG	TGACAGCAGC	180
AGGCACATCG	GCTTGTTTAG	GCTCCTCCTT	GGCTGGGGCA	TCTTCAGCCT	TGGAGGACGG	240
CGAGTTATCA	GTGGAAGCTT	TAGTGGCACT	TTCTGTCTCA	GCTGAGCCGG	CCTTCTCCTC	300
TGAGGATGCA	GGAGCCTGGG	GGGCTACCTG	CTCTGTGGCA	GCATCACCCCT	CCCCCTTTTT	360
CTCCTCGGAA	GGAGTTTCTC	CTGCTTTGCC	GGGCTCATCA	GGCTTGGAGC	CAGTGGCTGG	420
GGCTGCTTCG	GCAGTAGTGG	TGCCTTCTCC	CTTCTTCTCC	ACCCCATCGC	TCGAG	475

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GTGCTGGCGG	ACATGGACGT	GGTGAATCAG	CTGGTGGCTG	GGGGTCAGTT	CCGGGTGGTC	60
AAGGAGCCCC	TCGGCTTTGT	GAAGGTGCTG	CAATGGGTCT	TCGCCATCTT	CGCCTTTGCC	120
ACATGCGGCA	GCTACAGTGG	GGAGCTCCAG	CTGAGCGTGG	ATTGTGCCAA	CAAGACCGAG	180
AGTGACCTCA	GCATCGAGGT	CGAGTTCGAG	TACCCCTTCA	GGCTGCACCA	AGTGTACTTT	240
GATGCACCCA	CCTGCCGAGG	GGGCACCACC	AAGGTCTTCT	TAGTTGGGGA	CTACTCTCTG	300
TCAGCCGAAT	TCTTTGTCAC	CGTGGCCGTG	TTTGCCTTCC	TCTACTCCAT	GGGGGCTCTG	360
GCCACCTACA	TCTTCCTGCA	GAACAAGTAC	CGAGAGAATA	ACAAAGGGCC	CATGCTGGAC	420
TTTCTGGCCA	CGGCTGTGTT	CGCCTTCATG	TGGCTAGTTA	GCTCATCGGC	ATGGGCCAAG	480
GGGTGTCTAG	ATGTGAAGAT	GGCCACAGAC	CCAGATGAAC	TCGAG		525

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GCAAACAGAC	AAGGCTTACA	GGTTAGTTCA	GGATCTGCGC	CTTATCAAGC	AAATTGTTTT	60
GCCTATCCAA	CCTGCGGTGC	CAAACCCATA	TACTCTCCTA	TCCTCAATAC	CTCCCTCCAC	120
AACCCCTCCA	TAACCCATTA	TTCGGTTCTG	GATCTCAAAC	ATGCTTTCTT	TGCTATTCTT	180
TTGCATCCTT	CATCCCAGCC	TCTCTTTGCT	TTCACTTGGG	CTGGCCCTGA	CACCCATCAG	240
CCTCAGCAAC	TTACCTGGGC	TGTACTGCCA	CAAGCCTTCA	CGGACAGCCC	CCATTACTTC	300
AGTAGCCCTC	GAG					313

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

```

GAGACTATCG CCTATACTTT ATTTGGGTAA ATGTTTGGT TAAGGTTGTT TGGTGGTAGC      60
TGGTTGGGTT GCTGGGGCTC GGTGTGTGTA GTCGCGATGT TCTTCTCCGA GGCCAGAGCC      120
AGGTCGCGGA CGTGGGAAGC CAGTCCCTCG GAACACAGGA AGTGGGTGGA AGTATTTAAA      180
GCATGTGATG AAGATCACAA AGGATATCTC AGCAGAGAGG ACTTTAAAAC TGCTGTTGTA      240
ATGCTGTTTG GGTACAAGCC CTCCAAGATA GAAGTGGATT CTGTGATGTC TTCAATAAAT      300
CAAATACTT CTGGTATATT ACTCGAG                                           327

```

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

```

GCCTGCCCCC ACCTTACAGG TCTGGGATGT ACCTTTCCAT CTGTTGCTGC TTTCTTCTAT      60
GGGCCCCTGC CCTCACTCTC AAGAACCTCA ACTACTCCGT GCCGGAGGAG CAAGGGGGCCG      120
GCACGGTGAT CGGGAACATC GGCAGGGATG CTCGACTGCA GCCTGGGCTT CCGCCTGCAG      180
AGCGCGGCGG CGGAGGGGCG AGCAAGTCGG GTAGCTACCG GGTGCTGGAG AACTCCGCAC      240
CGCACCTGCT GGACGTGGAC GCAGACAGCG GGCTCCTCTA CACCAAGCAG CGCATCGACC      300
GCGAGTCCCT GTGCCGCCAC AATGCCAAGT GCCAGCTGTC CCTCGAG                                           347

```

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

```

GGTAGGACCG GCGAGGAATA GGAATCATGG CGGCTGCGCT GTTCGTGCTC CTGGGATTCG      60
CGCTGCTGGG CACCCACGGA GCCTCCGGGG CTGCCGGCAC ATTCTTCACT ACCGTAGAAG      120
ACCTTGGCTC CAAGATACTC CTCACCTGCT CCTTGAATGA CAGCGCCACA GAGGTCACAG      180
GGCACCGCTG GCTGAAGGGG GGCGTGGTGC TGAAGGAGGA CGCGCTGCCC GGCCAGAAAA      240
CGGAGTTCAA GGTGGACTCC GACGACCACT GGGGAGAGTA CTCCTGCGTC TTCCTCCCCG      300
AGCCCATGGG CACGGCCAAC ATCCAGCTCC ACGGGCCTCC CAGAGTGAAG GCTGTGAAGT      360
CGTCAGAACA CATCNACGAG GGGGAGACGG CCATGCTGGT CTGCAAGTCA GAGTCCGTGC      420
CACCTGTCAC TGA CTGGGCC TGGTACAAGA TCACTGACTC TGAGGACAAG GCCCTCATGA      480
ACGGCTCCGA GAGCAGAGTT CTCGAG                                           506

```

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

```

GAATTCCTCT TCTTTACCT CGTCCTGCCG GGCACCTTCC TTAGGTTTGG TTTTCATCTAC      60
AGCTTCTATG TTCTCTTCAG CTGGGCTGCT CTCCCCAGTC TCCGTTGGAG GCTGGGCTGT      120
TGCTTGGCA GCAGCATCCT CTGCGGCAGG GGTGGTGGCA GCAGCAGCAG TGACAGCAGC      180
AGGCACATCG GCTTGTTTAG GCTCCTCCTT GGCTGGGGCA TCTTCAGCCT TGGAGGACGG      240
CGAGTTATCA GTGGAAGCTT TAGTGCCACT TTCTGTCTCA GCTGAGCCGG CCTTCTCCTC      300
TGAGGATGCA GGAGCCTGGG GGGCTGCCTG CTCTGTGGCA GCATCACCTT CCCCCTTCTT      360
CTCCTCGGAA GGAGTTTCTC CTGCTTTGCC GGGCTCATCA GGCTTGGAGC CAGTGGCTGG      420
GGCTGCTTCG GCAGTAGTGG TGCCTTCTCC CTTCTTCTCC ACCCATCGC TCGAG      475

```

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

```

GAATTCGCCT TCATGGCCTA CAAGCTCTAG CCTAGACCTT TAGTGTGCCA TGCAGTCACA      60
GGTCTGAAAA GCAGCATCAT CCAAACCTTA CTTAATCTCT AAAATCTCAG CTGGTGGACA      120
GCTCATGATT AGTTCAGCCC ACTTCCTCCC CCTTAGTTGA GTTTGCAGCA GGACGCAGGA      180
GATAAGCACT TCCAAGCAAG TCTGATTAT ATATCAAACCT CGGTCTCCAT CCCAGGCCAG      240
CTGACCCTCA GAGCCAGCAA TGCTCTGTGC TTCCTCCCTG CGTCACGGCT TGGCAAGAGC      300
TGCTCTGCT GAGCAGTGTG TGTGATGGAG ACGGAGGCCG CTGAAGGCCG AGTGCTTGCA      360
GGCTTGTGAA CTGCCATCGA ACACAATCCA AACTCTGGAA ATGTTCTGTA CCACCTAAGC      420
CCTCAACAAC GTAATGCCTG TATGTGCTNT TTNTCAGTAA ACTCCTTGCT CATGTCNATA      480
AAGTATCCCT GAACACTCGA G                                501

```

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

```

GCGGGCACCA TTTCCAGTAT GTACCAAACC AAAGCCGTCA TCATTGCAAT GATCATCACT      60
GCGGTGGTAT CCATTTCAGT CACCATCTTC TGCTTTCAGA CCAAGGTGGA CTTCACCTCG      120
TGCACAGGCC TCTTCTGTGT CTTGGGAATT GTGCTCCTGG TGACTGGGAT TGCTACTAGC      180
ATTGTGCTCT ACTTCCAATA CGTTTACTGG CTCCACATGC TCTATGCTGC TCTGGGGGCC      240
ATTTGTTTCA CCCTGTTCTT GGCTTACGAC ACACAGCTGG TCCCGGGGAA CCTCGAG      297

```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

```

GCTCCACCAG CTACTGAGAA AATGGCCTGT AAAGATCCAG AAAAACCCAT GGAGGCCTGT      60
GCCTCAGCAC ATGTGCAACC CAAGCCTGCC CCTGAAGCCA GTAGCCTAGA GGAGCCCCAT      120
AGCCAGAAA CAGGGGAGAA GGTAGTAGCA GGAGAGGTAA ACCCACCCTAA TGGCCCTGTG      180
GGGACCCAC TGAGCCTCTT GTTGGGGAT GTGACATCCC TGAAAAGCTT TGATTCATTG      240
ACAGGTTGTG GTGACATAAT AGCAGAACAA CTCGAG                                276

```

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

```

GAATTCGGCC TTCATGGCCT AGCCAGACAA CTTGTACTGA TCTTTCTTTG CTTGCCTAC      60
TAATCACACA CACCTCTCTT TCTAGCCTGT GAAGACTTAA CTGATTTTCT ACGGATGAAG      120
GTTTCAGTGT CCAAGGCC CATACCGTAT CTGATTTTAC TTTATTTTGT TTTGTTAAGC      180
CTAACAGCTT CTGAGGAGCC ACGTAGAGCT CAAGAAGCAA AAGCTACTGA GAGTAGATGC      240
TATGTAAACT GCACAAGACG TCTCGAG                                267

```

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

```

GAATTCGGCC TTCATGGCCT AAAAAAGAT GCTGGACAAG GCGTTTGAG AGCGGATCAT      60
CCATGACTAC AAGGATATTT TCAACAAGC AACTGAAGAC AGGCTCACCA GTGCCAAGGA      120
ACTGCCCTAT TTTGAAGGTG ATTTCTGGCC CAATGTGTTA GAAGAGAGCA TTAAGGAACT      180
AGAACAAGAA GAAGAGGAGA GGAAAAAGGA AGAGAGCACT GCAGCCAGTG AAACCACTGA      240
GGGCAGTCAG GCGACAGCA AGAATGCCNA GAAGAAGAAC NACNAGAAAA CCAACAAGAA      300
CAAAAGCAGC ATCAGCCGCG CCAACAAGAA GAAGCCAGC ATGCCCAACG TGCCAATGA      360
CCTGTCCCAG AAATCGAG                                379

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

```

GAATTCGGCC TTCATGGCCT ACATAATTG AATCAACACA ACCACCCACA GCCTAATTAT      60
TAGCATCATC CCTCTACTAT TTTTAAACCA AATCAACAAC AACCTATTTA GCTGCTCCCC      120
AACCTTTTCC TCCGACCCCC TAACAACCCC CCTCCTAATA CTAACCTACCT GACTCCTACC      180
CCTCACAATC ATGGCAAGCC AACGCCACTT ATCCAGTGAA CCACTATCAC GAAAAAACT      240
CTACCTCTCT ATACTAATCT CCNNACAAAT CTCCTTAATT ATAACATTCA CAGCCACAGA      300
TCTCGAG                                         307

```

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

```

GGATGGCGCC GCGGAGGGTC AGGTCGTTTC TGCGCGGGCT CCCGGCGCTG CTAAGTGTGC      60
TGCTCTTCCT CGGGCCCTGG CCCGCTGCGA GCCACGGCGG CAAGTACTCG CGGAGAGAAGA      120
ACCAGCCCAA GCCGTCCCCG AAACGCGAGT CCGGAGAGGA GTTCCGCATG GAGAAGTTGA      180
ACCAGCTGTG GGAGAAGGCC CAGCGACTGC ATCTTCCTCC CGTGAGGCTG GCCGAGCTCC      240
ACGCTGATCT GAAGATACAG GAGAGGGACG AACTCGCCTG GAAGAACTA AAGCTTGACG      300
GCTTGACGA AGATGGGGAG AAGGAAGCGA GACTCATACG CAACACACTC GAG              353

```

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

```

GGATACCCCTA AAAAAACAAT CTATGTCAGA GGCTTCACTG GAGGTTACGT CACGTTATCG      60
TATTAATTTA GAAGATGAGA CACAGGATTT AAAGAAGAAA TTAGGTCAAA TCAGAAATCA      120
ATTGCAAGAA GCACAGGATC GACATACAGA AGCTGTCAGA TGTGCTGAGA AGATGCAAGA      180
TCACAAGCAA AAGCTTGAAA AAGATAATGC CAAGTTAAAA GTTACAGTCA AAAAGCAAAT      240
GGACAAAATT GAGGAGCTTC AGAAAAACCT GTTAAATGCA AATTGTCTG AAGATGAAAA      300
GGAAGTCGAG                                         310

```

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

```

GTTTGGATGA TTGGTGGCGT GTACGCAGCT GCTATGGCCT GGGCCATCAT CCCCCTAT      60
GGGTGGAGTT TTCAGATGGG TTCTGCCTAC CAGTCCACA GCTGGAGGGT CTTCGTCCTC      120

```

GTCTGCGCCT TTCCTTCTGT GTTTGCCATT GGGGCTCTGA CCACGCAGCC TGAGAGCCCC 180
 CGTTTCTTCC TAGAGAATGG AAAGCATGAT GAGGCCTGGA TGGTGCTGAA GCAGGTCCAT 240
 GATACCAACA TGCAGGCCAA AGGACATCCT GAGCGACTCG AG 282

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GAATTGGGCC TTCATGGCCT AGAACTTGT ACACCATGGA ATGTTCTACT TATTATTTTG 60
 TGCTACAATA TGTGCTGTTT CTTTGTGTTG AATTGCAGAT TGTCTACTAT GAAGCAGGGA 120
 TTATTTCTATG CTGTGTCCTG GGGCTGCTGT TTATTATCTT GATGCCTCTG GTGGGGTATT 180
 TCTTTTGTAT GTGTCGTTGC TGTAACAAAT GTGGTGGAGA AATGCACCAG CGACAGAAGG 240
 AAAATGGGCC CTTCTGAGG AAATGCTTGT CAATCTCCCT GTTGGTGATT TGTATAATAA 300
 TAAGCATTGG CATCTTCTAT GGTTTTGTGG CAAATCACCA GGTAAGAACC CGGATCCTCG 360
 AG 362

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

TCGAGGGACA TGAGGCTGAG CTGGTTCCAG GTCCTGACAG TACTGTCCAT CTGCCTGAGC 60
 GCCGTGGCCA CGGCCACGGG GGCCGAGGGC AAAAGGAAGC TGCAGATCGG GGTCAAGAAG 120
 CGGGTGGACC ACTGTCCCAT CAAATCGCGC AAAGGGGATG TCCTGCACAT GCACTACACG 180
 GGGAGCTGG AAGATGGGAC AGAGTTTGAC AGCAGCCTGC CCCAGAACCA GCCCTTTGTC 240
 TTCTCCCTTG GCACAGGCCA GGTCAATCAAG GGCTGGGACC AGGGGCTGCT GGGGATGTGT 300
 GAGGGGGACC TCGAG 315

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTTTAAT TAAGAATTGG GCCTTCATGG CCTAATCGAG GAGAATGGAG ACCAAACCTG 60
 TGATAACCTG TCTCAAAACC CTCCTCATCA TCTACTCCTT CGTCTTCTGG ATCACTGGGG 120
 TGATCCTGCT GGCTGTTGGA GTCTGGGGCA AACTTACTCT GGGCACCTAT ATCTCCCTTA 180
 TTGCCGAGAA CTCCACAAAT GCTCCCTATG TGCTCATCGG AACTGGCACC ACTATTGTTG 240

```

TCTTTGGCCT GTTTGGATGC TTTGCTACAT GTCGTGGTAG CCCATGGATG CTGAAACTGT      300
ATGCCATGTT TCTGTCCCTG GTGTTCCCTG CTGAGCTCCT AGCTGGCATT TCAGGGTTTG      360
TGTTCGTCA TGAGATCAAG GACACCTTCC TGAGGACTTA CACGGACGCT ATGCAGACTT      420
ACAATGGCAA TGATGAGAGA ATGCTCGAG                                         449

```

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

```

GGGCTTTAAA GGCAGACATT GATGCTACAT TATATGAACA AGTCATCCTG GAAAAAGAAA      60
TGGGAACCTTA TTTGGGCACC TTTGATGATT ACTTGGAGTT ATTCCTGCAG TTTGGTTATG     120
TGAGCCTTTT CTCCTGTGTT TACCCATTAG CAGCTGCCTT TGCTGTGTTA AATAACTTCA     180
CTGAAGTAAA TTCAGATGCC TTA AAAATGT GCAGGGTCTT CAAACGTCCA TTCTCAGAAC     240
CTTCAGCCAA TATTGGTGTG TGGCAGTTGG CTTTGTAAAC GATGAGTGTG ATATCTGTGG     300
TCACTAACTG TGCCTGATT GGAATGTCAC CACAAGTGA TGCAGTCTTT CCAGAATCAA     360
AGGCAGACCT CGAG                                                         374

```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```

GTACAATCTG AATCCAGGTC TGACAGCTGG CCATACAAAG TCATACTTTC CCCACATCCC      60
TCCTCTTTGA TAGGCATTGT CATCTAGAGC AATAGCCTCG AAATAGACTG AACACCGTGG     120
CCCATAGCTT AACTCCGTTT CACCTCTATT TCAAAGTAAA CTTGGGCTGG GATTACAGGC     180
ATGAGTATGT TTTCAATTGT ACATAAAGAC TTTATACAAA TGCTCTTCCT AATATTGCT      240
ACTTATTTT GCATTAGTTC AAATCTTTG TCCTGTCATC CCAAACTCT CGAG                294

```

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```

GAATTCGGCC TTCATGGCCT AACTGCACG GGGAACCCCC GAACCATCAT CGTGCCACCC      60
CTGAAAACCC AGGCCAGCGA AGTATTGGTG GAGTGTGATA GCCTGGTGCC AGTCAACACC     120
AGTCACCACT CGTCCTCCTA CAAGTCCAAG TCCTCCAGCA ACGTGACCTC CACCAGCGGT     180
CACTCTTCAG GGAGCTCATC TGGAGCCATC ACCTACGGG AGCAGCGGCC GGGCCCCCAC      240

```

TTCCAGCAGC AGCAGCCACT CAATCTCAGC CAGGCTCAGC AGCACATCAC CACGGCCGTC 300
GAG 303

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GCCACAAGCC TGTCAGCAAG TGGGGCTACT TGGGTCTCG GGCCTCAATC CACTCCTGGC 60
CAGAGACAAC TTCCTCTCCC ATGGGAAAGG CTAACGCATG CCCATAAATT AAGACATTG 120
CTCTCCCTCC AAGCCCTGGA AACCTGGGAC TCTCTAACAT CTACCTCTGT TTTCTTTGGC 180
TGCATTCAAC TTTCTGCAA TTAGTCAGGC CCTGGGGCAG CAGTTAGACG ACAGATGAGT 240
CAGAGGATTG CAGAATCTAA TCCAGAAGGA AGAGTTTATC CAAATGTTGG TGGCCTTTCT 300
CTTTTGGCGC ATTCTCTTCT GGTCTGTCT TTTCTCAGGA GTCTCTGAG CTTCATGTA 360
CCGGGCCCCC TCGAG 375

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GCAAGGGCAG GCGGGTCCCC CAGTCCCGCC ATTACGGGT GTCAGACCGT CTGCGTGTGG 60
CAGGGCTCCC AAGGGCAGGC GGGTCCCCCA GTCCCGCCAT TACGGGTGTG CAGACCGTCT 120
GCGTGTGGCA TTTTGTGGCT TATAAGCTTC ACCCACTCAC CCCCAACCCA CACCCACAT 180
CCCCCTGCCG GCAGCCCTC AACCTAAGAA GGCCAGAGCA TATTATTATT TGGAGGGAGC 240
AGATTACTTC TCCCAGAGAA AGGAAAATCT TGGAAAAGAT TAAAAACAC AAATCTAAGC 300
CTGACGGTT TTTTGTCCC TTTTGACCCC CTTCCCATTT TTTAGNATT TATTTCCATG 360
GCTTTTTTTT TTCTGTGCG TGTCTCGAG 390

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

GAATTCGGCC AAAGAGGCCT AAGCAGGCGC GAGGCGGCGG CAGCGAGCCG GGTCCCACCA 60
TGGCGCGGAA TTATTCCAGT ACCAGTACCC GGAGAGAACA TGTCAAAGTT AAAACCAGCT 120
CCCAGCCAGG CTTCTGGGAA CGGCTGAGCG AGACCTCGGG TGGGATGTTT GTGGGGCTCA 180
TGGCCTTCCT GCTCTCCTTC TACCTAATTT TCACCAATGA GGGCCGCGCA TTGAAGACGG 240

```

CAACCTCATT GGCTGAGGGG CTCTCGCTTG TGGTGTCTCC CGACAGCATC CACAGTGTGG      300
CTCCGGAGAA TGAAGGAAGC TGGTGCACAT CATTGGCGCC TTACGGACAT CCAAGCTTTT      360
GTCTGATCCA AACTATGGGG TCCATCTTCC GGCTGTGAAA CTGCGGAGGC ACGTGGAGAT      420
GTACCAATGG GTAGAAACTG AGGAGTCCAG GGAGTACACC GAGGATGGGC AGGTGAAGAA      480
GGAGACGAGG TATTCTTACA ACACTGAATG GAGGTCAGAA ATCATCAACA GCAAAAACCTT      540
CGACCGAGAG ATTGGACACA AAAACCCAG TGCCATGGCA GTGGAGTCAT TCATGGCAAC      600
AGCCCCCTTT GTTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

```

GAATTCGGCC AAAGAGGCCT AGGACTTGTT TCGGAAGGAG CTGACTGGCC AATCACAATT      60
GCGAAGATGA AGGCTCTGTG GGCCGTGCTG TTGGTCACAT TGCTGACAGG ATGCCTAGCC      120
GAGGGAGAGC CGGAGGTGAC AGATCAGCTC GAGTGGCAAA GCAACCAACC CTGGGAGCAG      180
GCCCTGAACC GCTTCTGGGA TTACCTGCGC TGGGTGCAGA CGCTGTCTGA CCAGGTCCAG      240
GAAGAGCTGC AGAGCTCCCA AGTCACACAA GAACTGACGG CACTGATGGA GGACACTATG      300
ACGGAAGTAA AGGCTTACAA AAAGGAGCTG GAGGAACAGC TGGGTCCAGT GCGGAGGAG      360
ACACGGGCCA GGCTGGGCAA AGAGGTGCAG GCGGCACAGG CCCGACTCGG AGCCGACATG      420
GAGGATCTAC GCAACCGACT CGGGCAGTAC CGCAACGAGG TGCACACCAT GCTGGGCCAG      480
AGCACAGAGG AGATACGGGC GCGGCTCTCC ACACACCTGC GCAAGATGCG CAAGCGCTTG      540
ATGCGGGATG CCGAGGATCT GCAGAAGCGC CTAGCTGTGT ACAAGGCAGG GGCAGTCGAG      600

```

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

```

GAATTCGGCC TTCATGGCCT AGTATTTCCT TATCACAGAT TTTGGGAGCA ACAGTGTTTT      60
CCCATCTGGA GGAGGGTGAG TTAATTCTGT GGAACACCCA TTTGGTTGGA AATAAAAACA      120
CAGCATGGAT TTAATTCATG CCACTTATTT ATTTTATTA GGACTTGAGC TTCTTTGTAT      180
TTTTTTTGCT TTGCTTCCAC TCAAAACCAG ATTTGGTGGT TGCTGTGTAA ACAGTGAAAT      240
ACAACACAGG CCAGGACTCG AG

```

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

```

GAATTCGGCC AAGAGGCCTA GTATTCTTTC GTTCTCTCT AAAAGAAGAA AAATATAATT      60
TAGAAATACA TTGCGTATTT TCTAAAACAA TAAATTTATA GTGTTAATAT TCATAGGGTC      120
AATCAAAATG AAGCTTCTCC TTTGGGCCTG CATTGTATGT GTTGCTTTTG CAAGGAAGAG      180
ACGGTTCCCC TTCATTGGTG AGGATGACAA TGACGATGGT CACCCACTTC ATCCATCTCT      240
GAATATTCCT TATGGCATA GGAATTTACC ACCTCCTCTT TATTATCGCC CAGTGAATAC      300
AGTCCCCAGT TACCCTGGGA ATACTTACAC TGACACAGGG TTACCTTCGT ATCCCTGGAT      360
TCTAACTTCT CTGGATTCC CCTATGTCTA TCACATCCGT GGTTTTCCT TAGCTACTCA      420
GTTGAATGTT CCTCTCTCC CTCCTAGGGG TTTCCCGTTT GTCCTCGAG      470

```

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

```

GAATTCGGCC AAAGAGGCCT ATGCAGATTC TGTGGTTATA CTCACTCCTC ATCCCAAAGA      60
ATGAAATTTA CCACTCTCCT CTTCTTGGCA GCTGTAGCAG GGGCCCTGGT CTATGCTGAA      120
GATGCCTCCT CTGACTCGAC GGGTGTCTGAT CCTGCCCAGG AAGCTGGGAC CTCTAAGCCT      180
AATGAAGAGA TCTCAGSTCC AGCAGAACCA GCTTCACCCC CAGAGACAAC CACAACAGCC      240
CAGGAGAGTT CGGCGGCAGC AGTTCAGGGG ACAGCCAAGG TCACGTCAAG CAGGCAGGAA      300
CTAAACCCCC TGAAATCCAT AGTGGAGAAA AGTATCTTAC TAACAGAACA AGCCCTTGCA      360
AAAGCAGGAA AAGGAATGCA CGGAGGCGTG CCAGGTGGAA AACAATTCAT CGAAAATGGA      420
AGTTCCTCG AG                                     432

```

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

```

GAATTCGGCC AAAGAGGCCT AAAAAGTATA TACATTTTAG TACTGCTTTG ATTTTGTTTA      60
CATACTGAAA AATGTATCTG AAAATGAGTT ATTTTGGACT CGAG                          104

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

```

GAATTCGGCC AAAGAGGCCT ATTCACCTCA GCTTCACTGA CTTCTGGATT CTCCTCTTGA      60

```

```

GTAAAAGGAC TCAGCCAACT ATGAAGTTTT TTGTTTTTGC TTAAATCTTG GCTCTCATGC      120
TTTCCATGAC TGGAGCTGAT TCACATGCAA AGAGACATCA TGGGTATAAA AGAAAATTCC      180
ATGAAAAGCA ACATGATCTC GAG                                          203

```

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

```

GAATTCGGCC ACAGAGGCCT AGCCAGTCT CGGGTATGTC TTTATCAGCA GCATGAAAAT      60
GGACTAATAC AGTTGCTATG ATTATTAGTT TTTTGCTACT GAGTTGTAGG AGTATCTGAT      120
ATATATTTTG GTAACAAATC CCTTATAAAA TATATTGTTT CCAAATATTT TTTTCCCAT      180
CCATAGGCTG CCTTTTCATT CTGTTGTTTC CTTTGCTTCA GGTAAGGGAT TCTGAAACAA      240
CTATTGCGGC AGCAGAACAG CTTCTTTTGT TTGCTTTCTC ATTGTCTACT GTGTTCTGCA      300
TAAATAAGGT TATGAATTAG CTGTTGTTCA TATGGGTGAA AGATTTGCAT CTGTGGACGC      360
TTAGATAGCA CATATGGTAA ACCATAGAAC TTCACCATT ATAACCTTTG AACAACTGAT      420
ACACTTAGAA AAGCAGTTTT TGGCTGGGCG CGGTGGCTCA TGCCTGTAAT CCCTAGGCCT      480
CGAG                                          484

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

```

GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCCT CGAGCTGACA ACTATGAAGT      60
TTTTTGTTTT TGCTTTAATC TTGGCTCTCA TGCTTTCCAT GACTGGAGCT GATTCACATG      120
CAAAGAGACA TCATGGGTAT AAAAGAAAAT TCCATGAAAA GCATCAAGGA CTCGAG      176

```

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

```

GAATTCGGCC AAAGGGCCTA ATTTTATTAA TAACATTTTA AAAACAACAA TTATGAAAAA      60
GCAATTCGGT TTACCGCTGA TGCTTGCGTC AGCCCTCGCC TTCTCTGCTT GTAGCTCTGA      120
TGATGTGGCC GAGAATGGCC CAAAGGACAT CGCAGCTCTT ACAGATGGTG GTTACTTGAA      180
GATGTCTATC AATCTTCCTT CCCGTGCTGC TAATGGTGGC TTCAGAGCTA CGGAACAAGA      240
CGGTTATGTT AACTTGGAAG ATGGATTGGC AAAAGAGTAC AATGTAAAGG ATGCTATCCT      300

```

CGTCCTTTTC CAAGGTGATA ATGAAGCAGA TGCCAAGTTC CATTCTGCAT ATGAACCTTAC	360
TACATCAATG CAGAAGGATG GCTCTACGCA AATCACTTCC ACAACGAAAC TTGTTAAGAA	420
TGTGAATATT GGTGGTCAGG GAAATCCTCT TAAACCTGCT GATGTTAAGC TCGAG	475

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GAATTCGGCC AAAGAGGCCT ACAATTATGG GGCTTATGGG GAACATGCTC ATTGTGTTTT	60
ACCAATCAGG ACATGGAAC TAAACAATAT TTGTTGACTT ATAGTGAAC CTGGCTAATT	120
AGGACTCTTA ACCAGCACTC TTAATTAAC TACTTATTT TCTCTGTGTC CACCCCTCTT	180
AAAGAAAAAG AAGCGAACT CGAG	204

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGTAG GCCTCTTTGG CCGATTGAAT	60
TCTAGACGCG GCTCGAGGCA GGTCTAGGCC TCTTTGGCCG AA	102

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GAATTCGGCC AAAGAGGCCT ACTCAATTGT TCCTTTCTTC CATCACCACC CTTTGAAGGT	60
CTCTTTGCCT ACTTGTAGAT TTAGGGGGAC ATAACATTGA GACTGAGCAG TTTCTTGAAC	120
CTCTCCTCTC AGCAGCCACC AGCCTGGCTT TCGCAGACCA CTGGAAAGTA TCCCAGCTCA	180
TTAGCTTTTG GAATGACGGG AAGCCTTTTG ATGTTNGACG TCTTAATCTC AACTCTTCAA	240
CTTAGCTCAT TCTGGAGCAG TCACGGGATG ACAGATGAGC TCGAG	285

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GATAACTTGA	GATCAAATCA	GTCATATTTG	ACTCTTCTCT	TTTTCACCTC	TTTTATATCT	60
GATCAGTCAG	CAGTTTTTTG	AAACCCTGTT	CGAAGCAGTT	CTCAACACTT	GTGCACCCAT	120
TCTTCTCTCT	ACACCACTCA	ATCTAGACCC	TCACATGTGG	CTGTCCTGCT	TTCTTCTCT	180
CCTACTTCTA	AGCTATTCTG	TGGAGAGATG	TCAAAGTAAT	CTTCACAAAA	AATCTGATTG	240
CATCACTTCA	CATCTCGAG					259

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GGGCTTTAAA	GGCAGACATT	GATGCTACAT	TATATGAACA	AGTCATCCTG	GAAAAAGAAA	60
TGGGAACCTA	TTTGGGCACC	TTTGATGATT	ACTTGGAGTT	ATTCCTGCAG	TTTGGTTATG	120
TGAGCCTTTT	CTCCTGTGTT	TACCCATTAG	CAGCTGCCTT	TGCTGTGTTA	AATAACTTCA	180
CTGAAGTAAA	TTCAGATGCC	TTAAAAATGT	GCAGGGTCTT	CAAACGTCCA	TTCTCAGAAC	240
CTTCAGCCAA	TATTGGTGTG	TGGCAGTTGG	CTTTTGAAAC	GATGAGTGTT	ATATCTGTGG	300
TCACCTAAGT	TGCGCTGATT	GGAATGTCAC	CACAAGTGAA	TGCAGTCTTT	CCAGAATCAA	360
AGGCAGACCT	CGAG					374

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCGGCC	TTCATGGCCT	AGATAAGTAA	ATAGACTTAC	AGAGGGAAAG	TAACTTGGCT	60
AAGGTGAACT	TGAACCAAGA	TGACTGACTC	CAGAGCTTCC	ATTTTCTTTT	TTCTTTCTTT	120
TTTTTTTTTT	NGGAGACAGA	GTCTCACTCT	GTCGCCCAGG	CTGGAGTGCA	ACGGCGCGGT	180
CTCCACTCAC	TGCAGCCTCC	AGCTCCTGGG	CTCAAGTGAT	CCTCCACCT	CAGCACCCCC	240
ACGTCTCGAG						250

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

```
GAATTCGGCC TTCATGGCCT ACAGGGAGGG AGGGGTTCTG AGAGCCTCAG ACCACAGGGC    60
CTGAGGCCCA CAGTGGCCCA GAGTCCATCT GGCAGCCCCT GCTCTGCTGG CCCAGGGGGC    120
TCTCCCCAGG GTGGAGTAGG CAGGGGAGGG TCGCTGGTCC CCAGTCCCAG CCTTCGAGAG    180
GTGGGGCCAG ACAGCAGGGC ACCCGTACCC GAGACCACAG TGCTCCCCAA GGCCAGCTCT    240
CTCCCCAGTG AGGTCACTCC TACCTCCGGG GCCATTGTTGG GCGGGGGATC CTGTAGATCT    300
CTGACTCTGC GCGCCTTAT CTTGATGGCC TGGCNCAAGA AGGGAGGGCG CTGCCCCTT    360
CCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

```
TTTTGACTGA CTCTTTAAAT TAGTACAATT TTTCTACTTG TCATATAACT CCTGGAACAA    60
TAGTACGGGA AGCCGTGATC CTTTCCCTG ACTCATGATT TTAGTCTTTT TCCAAATCGC    120
TGTTTTTTTT TGGTTTTTTT TTTTITGCT GCTCCAACGA CCAGCATGTG TTGGAGCAGA    180
TCTCCATGGT AAGCCAAAAG TGGACTTGTC AGCCTATAAC TACTCTGCAG CTGCCACTAA    240
CTCTACAGGC ACAGAGCTCG AG
```

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```
CAGAAACTCT TGGACTCAAA AGAGAAAGAA AAAAGTCAAG CCAAGGAAAG CACAAGAGGT    60
AAGACAGGCC TAGTGATCTC AGCAGGCAGA ATTTATGGAC ATATTTTGCA GGCAAGTGGT    120
TCTCAATCAG GGGTGATTTT TGGCTTGTA AAGACATTTAG CAATATCTGG ACACATTTT    180
TGGTTGTCGT AAGTGGATGG GGGTTGCTGC TATCATCCTA CAATGCATAG GTGCATTAGT    240
CTGTTTTCAT GCTGCTGATA AAGACATACC GGAGACTGGG CAATTTGCAA ATGAGAGATG    300
GCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```

GAATTCGGCC TTCATGCCTA CAGCCATATT AAAACTAAGT AAACCTCGTCC CTGGGAACTA      60
CACTTTTCAGC TTGACTGTAG TAGACTCTGA TGGAGCTACC AACTCTACTA CTGCAAACCT      120
GACAGTGAAC AAAGCTGTGG ATTACCCCCC TGTGGCCAAC GCAGGCCCA ACCAAGTGAT      180
CACCCTGCCC CAAAACCTCA TCACCCTCTT TGGGAACCAAG AGCACTGATG ATCATGGCAT      240
CACCAGCTAT GAGTGGTCAC TCAGCCCAAG CAGCAAAGGG AAAGTGGTGG AGATGCAGGN      300
TGTTAGAACA CCAACCTTAC AGCTCTCTGC GATGCAAGAA GGAGACTACA CTTACCAGCT      360
CACAGTGAAT GACACAATAG GACAGCAGGC CACTGCTCAA GTGACTGTTA TTGTGCAACC      420
TGAAAACAAT AAGCCTCATC AGGCAGATGC AGGCCAGAT AAAGAGCTGA CCCTTCCTGT      480
GGATAGCACA ACCCTGGATG GCAGCAAGAG CTCAGATGAT CAGAAAATTA TCTCATATCT      540
CTGGGAAAAA CACAGGGACC TGATGGGTGC AGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```

GAATTCGGCC TTCATGGCCT AACTTTGTGT GATCAGAGTT TATGGGTGG GCTGCCCCAG      60
GCTTGGATAA CTTAAAGGCT TGATGAGGTC ATCAATTAT GCTTGGCTAC CCATGGCACA      120
GAAGCATAGC CCCACTGTGA TGGCTGGGGT GGCTCCGGG ATCCTGGGCA GTCAGGAGGA      180
AACTCCATGA AGGAAGGAGC TAACCTTTCT GGGGGTACCC CTATCCCAGC ACAGACTTCC      240
TCATCTCATT GGTGAGAACT GGGTCACATG AACATGCCTC AGCCTATCAC AGGCACAGGG      300
AATGAGACCA TCATGGACCA ATCAGGATTC ACCACTCAAG GTGGGGCCTG CCATCCGGAT      360
GGATGCTCTC CGCCACAGGG AGGTGGGGGA CCCAGAAGCT GTGGGCAATG GCCATGTGCA      420
CAGTAGGACT GAGGCACTCA GTCCCGTAGC TGACCTACCT GGGACAGGCC TGGAGGCTGA      480
CTTAGGTGTG AGGGGCAGAG AGATTACTGT GCACAGACCG CTGTGTGACC CCAGATCTAG      540
GTGGGATCCC GGTGTGCCCC ATCTGCCTGG CTTACCCCAA CCCCTCTGGA ACCTGAACCA      600
TTGAATTCTA GACCTGCCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

```

GAATTCGGCC TTCATGGCCT ACTCCAGAAT GAAGATCTTC TTGCCAGTGC TGCTGGCTGC      60
CCTTCTGGGT GTGGAGCGAG CCAGCTCGCT GATGTGCTTC TCCTGCTTGA ACCAGAAGAG      120
CAATCTGTAC TGCCTGAAGC CGACCATCTG CTCGACCAAG GACAACCTACT GCGTGACTGT      180
GTCTGCTAGT GCCGGCATTG GGAATCTCGT GACATTTGGC CACAGCCTGA GCAAGACCTG      240
TTCCCGGCC TGCCCATCC CAGAAGGCCT GCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GAATTCGGCC	TTCATGGCCT	AAGCTTTTGC	TTTTTTAATA	ACTTGTATAG	CTAAAAACTT	60
GACGGTGAAA	AGCTCTCAGA	TCAAAGCTGA	TCCTTCTGTC	AGTAATGATT	CTAAAAATAA	120
GCAAGATTTT	AATGGGGAAT	ATATTTTATT	TCATTCTTAT	CTCAAACCTA	GGTACTGTGG	180
TCGTTTTGAG	TTCATTTTCA	GGCATTTCAT	ATGTGCCTCA	GGCCACATCC	AACCTCTCCC	240
CAGAACTCGA	G					251

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GAATTCGGCC	TTCATGGCCT	ACAGTCTAAG	ACATTTCTTA	TTCTGCCTTC	TTGTCTTCCT	60
CCCTCTCTTC	CACATTGGTC	AGACTTACAT	CTTGGACAGC	TCTCCCAGCC	ATCTTCTACT	120
GCCTCCCTAT	TTTCCCTCC	CAGACTTTTC	CCGCAAAAC	ATCTGTGCA	GGTGGTATTA	180
ATTTCTATC	ACGGCTGTGA	CAAATTACCA	CAAACCTCAGT	GGCTTAAAC	AATGCACATT	240
TATTATCTGA	CAGTTCTCGA	G				261

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GAATTCGGCT	TCATGGCCTA	GCAAGACTCC	ATCTCAAAAA	AAGAAAGAAA	GAAAAAAGAA	60
AGTACAAGTT	TATAAAGTAT	TATAGTGAAA	AATTCGCATT	CTGGCTGATT	TTAAGCCATT	120
TAAAATTTAT	ATAAAACAAC	CTTCCATAAA	AATTTGACAG	GTGCCCAGAT	GTTGCTTTCT	180
CCATTTATTT	TTTGTTTTTT	TTTAATCACA	CTCGAG			216

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

```

GCGATTGAAT TCTAGACCTG CCTCGAGTAA GTGCCGAAAA CTTCACTGTG CTCATCAAGA      60
ACAATATCGA CTTCCCGGGC CACAACTACA CCACGAGAAA CATCCTGCCA GGTTTAAACA      120
TCACTTGTAC CTTCCACAAG ACTCAGAATC CACAGTGTCC CATTTCCTGA CTAGGAGACA      180
TCTTCCGAGA AACAGGCGAT AATTTTTCAG ATGTGGCAAT TCAGGTTGGT GGTGCTTTGT      240
ACACTGGGAT GTGGGGCTGT GTGTCTAGGG ATGGAGGATG TCAAACAAC TCGAG          294

```

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

```

GAATTCGGCC TTCATGGCCT ACCTTCACAG AAAAATGCAT AGCTGGATGC TGCAGACTCT      60
AGCGTTTGCT GTAACATCTC TCGTCCTTTC GTGTGCAGAA ACCATCGATT ATTATGGGGA      120
AATCTGTGAC AATGCATGTC CTTGTGAGGA AAAGGACGGC ATTTTAACTG TGAGCTGTGA      180
AAACCGGGGG ATCATCAGTC TCTCTGAAAT TAGCCCCCCC GATCTCGAG          229

```

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

```

GAATTCGGCC TTCATGGCCT AGCTTACTTT ACAATTCTGC TGTGTGTCAG GTGTTCTAT      60
AGTTTTTTTT AAAGGTATGT TAACTATTTT TCCCTTTTGG TTTATATTTG TAGGAATCTT      120
TGCTTTTAAG TGTGCCCCGTG CAGAAGAATT ATTTAATCATG TTGCAAGAGA TTATGCAAAA      180
TAATAGTATA AATGTGGAGC TCGAG          205

```

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

```

GAAGTGTAAT GTCAGACACA CAAGAAAAGC AAATCAGTGT TGTAAGCTTA AAGTACAATT      60
TCAAAGGTCA TTACCAACAG CAGGGTTTTT TTTATACTTT AAAACATTA TGCTACATAT      120
CATTGCCATT TTCATATTTT GGGGTTTTGC TACTCTTATA CAATGGAATC AATGGAAATG      180
TCATCCAGCC AGATCTCGAG          200

```

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

```

GAATTCGGCC TTCATGGCCT ACACAAATGT TTGTTGAGTG CTCATTGTAT GTCTGGAGAC      60
CATTCTGTCT TCTTCCCTAA GAGTGTTTCAT GCTGTTGGAC CAGGTGTTAT GATTTTGCTC      120
TGGAGAATAA GGTATTTCCA CATGGAGCAT GTGGAATAA TAGTGCCTAT CTCCTGAAAG      180
GTCCAGGTGA TGCAAGATG AATGAGACAT GATTGGAGGT TTTTCTTCTG TCTGAAATGC      240
AGACAGTTCT GGGTTGGGCA GCTCTGTAAG ATGCTGAACA TGTGTCCTTC CAAGAAGCAA      300
GGATCAGAAA GCAGACTC^A G                                     321

```

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

```

GAATTCGGCC TTCATGGCCT ACACCAATTGA CTTCTTCTAC CGGCCGCATA CCATCACCCT      60
GCTCAGCTTC ACCATCGTCA GCCTCATGTA CTTGCGCTTT ACCAGGGATG ACTCTGTTCC      120
AGAAGACAAC ATCTGGAGAG GCATCCTCTC TGTATTTTC TTCTTTCTTA TCATCAGTGT      180
GTTAGCTTTC CCAATGGTC CGTTCACGTC ACCTCATCCA GCCTTATGGC GAATGGTTTT      240
TGGACTCAGT GTGCTCTACT TCCTGTTCTT GGTATTCCTA CTCTTCCTGA ATTTCGAGCA      300
GGTTAAATCT CTAATGTATT GGCTAGATCC AAATCTTCGA TACGGCCACC TCGAG          355

```

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

```

GGAAACTTCT AGAAATAATG ACAAGGATTC AAACCTATTG TCAAATGAGT CCAATGTCAG      60
ATTTTGGAAC TCAACCCTAT GAACAATGGG CCATTCAAAT GGAAAAAAA GCTGCAAAAG      120
AAGGAAATCG CAAAGAACGT GTTGTGTCAG AACATTGAG GAAGTACAAT GAGGCCCTAC      180
AAATTAATGA CACAATTCGA ATGATAGATG CGTATACTCA TCTTGAACT TTCTATAATG      240
AAGAGAAAGA TAAGAAGTTT GCAGTCATAG AAGATGATAG TGATGAGGGT GGTGATGATG      300
AGTATTGTGA TGGTGATGAA GATGAGGATG ATTTAAAGAA ACCTTGAAA CTGGATGAAA      360
CAGATAGACT CGAG                                     374

```

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

```

GAATTCGGCC TTCATGGCCT AGAGAACTG AGAGGAAGTT AAAGATTTGT CTTACAAAGG      60
CTGTGTAGTG ATAAGACCTA AGGTTTTCTC TGAGATTCAA AATGGGTATT ATTTGTTCTT      120
TAATCCTTCT GATTATTCTT TTGGAAAAAA GGAAGTAGA GGAAAGGAAG TAGAAAAATA      180
ATATTCTTA TACTTATTAT GTACCAGACA TGGTGCTAAG TTCATTTAAA AACTGCCTC      240
ATTTAATCTT TGCAACCAAT TTATACCCAT ACACATAAGG CCACAAAAGC TCGAG          295

```

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

```

GAATTCGGCC TTCATGCCTA AGGTAAGGGA AAGTGAGAAG CAGCAGGATA GTCAGCCTGA      60
AGAAGTTATG GATGTGCTAG AGATGGTTGA GAATGTCAA CATGTAATG CTGACCAGGA      120
GGTAATGGAA ACTAATCGAG TTGAAAGTGT AGAACCTTCA GAAAATGAAG CTAGCAAAGA      180
ATTGGAACCA GAAATGGAAT TTGAAATTGA GCCAGATAAA GAATGTAAAT CCCTTTCTCC      240
TGGGAAAGAG AATGTCAGTG CTTTAGACAT GGAAAAGGAG TCTGAGGAAA AAGAAGAAAA      300
AGAATCTGAG CCCCAACCAC TCGAG          325

```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

GAATTCGGCC TTCATGGCCT ACAAGGACGT TAAAGGCATT TTATTCCAGC GTCTTCTAGA      60
GAGCTTAGTG TATACAGATG AGGGGTGCCG CTGCTGCTTT CCTTCGGAAT CCAGTGCTTC      120
CACAGAGATT AGCCTGTAGC TTATATTTGA CATTCTTCAC TGTCTGTTGT ATACCTACCG      180
TAGCTTTTTA CCGTTCACTT CCCCTTCCAA CTATGTCCAG ATGTGCAGGC TCCTCCTCTC      240
TGGACTTTCT CCAAAGGCAC TGGACCCTCG AG          272

```

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAATTCGGCC TTCATGGCCT AGCATCCCTG AAACTGTGTA ATTTTGAGGA TCCTTCTGGT	60
CTTAAAGCCA ATTTAGAAGG TGCTAATCTG AAAGGTGTGG ATATGGAAGG AAGTCAGATG	120
ACAGGAATTA ACCTGAGAGT GGCTACCTTA AAAAATGCAA AGTTGAAGAA CTGTAACCTC	180
AGAGGAGCAA CTCTGGCAGG AACTGATTTA GAGAATTGTG ATCTGTCTGG GTGTTAGCTC	240
GAG	243

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC TTCATGGCCT AAATTATACT CCAAATGTTT TATCTAAAAT GCATTTTCTG	60
TCTTTTCCTT TTTACTCTTG TCCTCACTTT TAATGATCCA TCGGCTGACA GTGTCTTTAC	120
ATCCAAAATG CAAAGCAGAC AAATGGGCAT ATCAGGGAAG AACATGACAA AAAGCACCAG	180
CATCAGTGGA GACATGTGCT CACTGGAGAA GAATGATGGC AGCCAGTCTG ACACTGCAGT	240
GGGCACCTTG GGCACCACTG GCAAAAAGCG GCGCTCTAGC CTGGTGCCA AAATGGTAGC	300
TATCGTTGGT CTGTCACGGA AAAGTCGCAG TGCTTCTCAG CTCAGCGGAC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCAAAT GCTTCAGGTA AATGTTGAAG CTCGGTGTAC CGCGGGACAA ATCCTGAGTC	60
ACCCCTGGGT GTCAGATGAT GCCTCCCAGG AGAATAACAT GCAAGCTGAG GTGACAGGTA	120
AACTAAAACA GCACTTTAAT AATGCGCTCC CCAAACAGAA CAGCACTACC ACCGGGGTCT	180
CCGTCATCAT GAACACGGCT CTAGATAAGG AGGGGCAGAT TTTCTGCAGC AAGCACTGTC	240
AAGACAGCGG CAGGCCTGGG ATGGAGCCCA TCTCTCCAGT TCCTCCCTCA GTGGAGGAGA	300
TCCCTGTGCC TGGGAAGCA GTCCCGGCC CCACCCCTCC GGAATCTCCC ACCCCGCTCG	360
AG	362

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

```
GAATTCGGCC TTCATGGCCT ACTCAGTCTG CACAACCTTT TTGCTGTGTG TCGGAATATG      60
TATAACTGGC TACTGCAGAA TCCCAAAAAT GTCTGTGTTG TCCACTGCTT GGATGGACGG      120
GCGGCATCAT CAATTCTGGT TGGTGCTATG TTCATTTTCT GTAATCTCTA CTCTACTCCT      180
GGCCCAGCCA TTCGATTGCT ATATGCAAAG CGACCAGGAA TTGACTTTC ACCATCCCAT      240
AGGAGATACC TGGGCTATAT GTGTGACCTA CTGGCAGACA AGCCCTACCG CCCTCGAG      298
```

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

```
GAATTCGGCC TTCATGGCCT ACCGTAAGCA GATGAAGCTG CTGCTGCTGC TGCTGCTGCT      60
GAGCTGCGCC GCGTGGCTCA CCTACGTGCA CCTGGGCCTG GTGCGCCAGG GACGCGCGCT      120
GCGCCAGCGC CTGGGCTACG GCGGAGATGG TGAGAAGCTG ACCAGTGAGA CCGACGGCCG      180
GGGGGTCCAC GCTGCGCCAT CCACACAGAG GGCTGAGGAC TCCAGTGAGA GCCGTGAAGA      240
GGAGACCAGC GCAGACATGC TCGGGCCAGA TCCCAGGGAT TACCTCGAG      289
```

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

```
GAGAGATGGT GACTGAGGCA GAAGCTAATA GGGAAGATGA TAGGAAAGAA ATTTTACCCA      60
AGGAATTAGA TTTAGCAAGA GAGCGAAGGA AAGCTGAGAG GCCAAAAACA TCTCTGAGGA      120
AAACTGACTC TGAGAGAGAA GAGGTGACAA GGGCAAATGC ACTCAAGGAT GAAGATGCTT      180
TTAAAGAAGA GCAAAAACCT AAAGCGGAAG AAGGGGAAAC AGAGACAGAA GTAAGAGCTG      240
AGGAAGAGAC AAAAGCTCCC CCAATGAAA TGGGATCTGA TGCTGAGAAC GAAACACTCG      300
AG                                                                                   302
```

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GAATTCGGCC TTCATGGCCT AGGATATTTA AACCTCTATT ATTTTAGACA AGACTGTCTA	60
GAACTTAAAGT TTGATCTGTC AGCCAGTACT CCCATTAAAT TCAGTGTAGT TTCACTTGAT	120
AGAATCAGAT ATGTTATCGA AATGTTAGCA GCAGCTTCAT CCTCCTTCTG ATTAAAGTAA	180
GTAGAAATGG GATGTTTGT TTAATAACAG CCATAGTGTG TGTTTAGACC ACAGCGGATG	240
TTGTAGACCA GGACCCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GAATTCGGCC TTCATGGCCT AGGGGCTTTT GTCAAGATAG AAGGGTATCA ACGGTTTCTG	60
TACAGCACAG ATTATGACAG CGTCTTCTT AAGACTTATC ATTTGGAGCA CTGGCTCAGG	120
AGTCGAAATC ACCAATGGCT CATCCATCAA TCAACCAGAA GTGAAGACGA AAGCTTCAAA	180
GAAGAGAATG TTAAATTTT ATCAAATGAA ACATATTTT GAAATACTTG ATAAATGAG	240
ATGCCTGAGA AAACGTTCTA CAGTGTCACT CTTGGGAGTT CTTGTCACTT TTCTCCTTTT	300
TATGAACTTG TACATTGAAG ATAGCTATGT TCTGGAAGGA GACAAACAAC TTATAAGGGA	360
AACTCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

GAATTCGGCC TTCATGGCCT ACTAACGACT CATCTTGTT TTTAGTTTTT TTAATTAACA	60
ATCGTTCTGT TCACAATTTT TAATTTCTT TCTTCCCCCT TCTCCGCAA GCACTCAGGC	120
ATCGGACACG CTATGGTAAA CAACTACAT TGTCTGGTAG ATATCATTCT TATTGTCTCT	180
TTTTTTGGGT TTGCCGTGTG TTGCCCCCT TTTCTCTCC AACCCCCC ATTCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GAATTCGGCT TCATGGCCTA GTGTATTGGT TGTGTGTGTT TTCCTTTTTC CATAAGAAAT	60
ATGTCCATTT AGTCCAGAGG CTCTTGCTTT ATCCGGATGA CGGAGGGTAC ACGGGGCGTC	120
CGCCTCAGTT CCCGCCGAG GACGTATTG CTGAAGTGGG ACGAGTCTAC TCCTCCCCCA	180
CAGGAGCCCA CGATTTCAAA TCCTCTTTCG TGCAACCTCT CGAG	224

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

```

GAATTCGGCC TTCATGGCCT AGATATTTTA AAGGAGTGAT GACATCTTTT TCCTATCATG      60
TGAAGAGGGG AAAGAGAAAG GAAAGGGCCC ATATTATTGT GTTCCTGCTT GTGCCAGCTG      120
TTCTATATCT GTTGATCTCA TTTAGTCCTC ATGACAGTTC TATGAGGAGG GCACTGTCAT      180
CATCACCATT GCACAGATGC AGAACTGTG GCTCACAGAG GATAAAGCTA GGTCACTCAC      240
ACAACCCCCT GACTCCAGAG CCACCACTCG AG                                     272

```

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

```

GAATTCGGCC TTCATGGCCT AGTAAGGGAG AACTGAATG GTGATTCAGA GCATAGAGAT      60
TATGTTTTTT TATGCACAGG GCTTCATCAG AAAAATGGAA GGAATTGTCA ATAACAATAA      120
AATGTTTCAGC TAGATCAACT CAGTATATAG TATGTATTAT ACAATTATTC AAAATAGTGT      180
TTAACAGTAC TGTAAATAACA TGAATAAATG TTTTGTCTATA TTAAGTGAAA AAGAGCTATA      240
TAAAATTATC TAAGTTTATG GTATATGTAG ATTGTTGCAA AAATGTCCTC AATTCTTTAT      300
CCCTCCCTGT ATCCACACCT GTATCAGTTT TCTCGGGGCA GCTGCCTCGA G                                     351

```

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

```

GAATTCGGCC TTCATGGCCT AGAATATTTT TATCATCCCA AAGCTAAAAC ATTAAAAAAT      60
TTAAAGTTTA TTCTTAGAGA TTGATGCAAC TTGCATATCT AATCGAG                                     107

```

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GGAAAATTAC TTAAACGTG CACACAACGT TTCACAAAAT CTTTGTGAA AGAAGAAAAG	60
GAAATTCAGT GTGTGAGTCT CAGCAGGAGT TAAGCTAATG CAGCTTAACA TCATGCCGAC	120
AAAGAAGCGC TTATCTGCGG GCAGAGTGCC CCTGATTCTC TTCCTGTGCC AGATGATTAG	180
TGCACTGGAA GTACCTCTTG ATCTGGTACA GCCTCCAACC ATCACCCTGC TAAATCCCCT	240
AGAAGTCCCA CTCCTAAACA CATCCGTATT ACTCGAG	277

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GAATTCAAAT TAACATTTTA CCTTGAATA GTTGGCTTCA GATTAAATATC AACTTAGTTT	60
CAATAGCATA GGAAATTTGC TTCACTATAT TTCCATTTC TCCCCGTCCT TTGTGCTATT	120
ATTACTATAC CAATTAGATC TCTACACAAT ATAGGCATAT CAACACATTT TGTAATTATT	180
TCCTTATCCA GTTGTCTTTT AATATAGATC TGTGAAGAAA AGTATTACAC AAATAGATCT	240
ATTCTGTTTT TTATAATTAT TTAATTACCT TTGGTGGTGC TGTTTATTTT TCATGCATTT	300
GAGTTACTGT CTAGTATTCA TTCATTTCTC TCTGAATCAC TCCCCGGTAT TGCTCGAG	358

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC TTCATGGCCT AGCCATCTTA TTTGAACTAT ATTTTTCCTT CAAAGAAGCA	60
ATAGGTCTCA ACATAGTGTA GGTAGCATCA GGTGACAGAA AGCCAATTTT ATTTTCAAAT	120
TTAAGTTAAT TATCTTCGTG ATCCTATTTA TCCACAATTT CTTTCAGAAA AGACTGAAAA	180
AACACATTAT ATTCAAGAGA TATAATGAAA TTATTGGAAG GCATCACTCG AG	232

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

```

GAATTCGCCC TTCATGGCCT AAATATTTTC CATCTTCCTC TCCAGTAAAC ATTCTTTTGT      60
CATCACAGTC TGTCTCTGAC ACCTTCGTTA AAGAGGTCTT AAAATGGAAA TATGAAATGT      120
TTTGAACATT TGGTCAGTGT GGGCCCCCTG CAAGTCTTTG TCAGTCCATC TCAAGACCTG      180
TGCTGTGAG ATTTCACAAT TATGGAGATT ATTTTAATGT TTTTTCCTT TTGATGGTAT      240
TGAATACTTT TGAACAGTG GCACAAGCGG CTCGAG                                276

```

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

```

GAATTCGGCC AAAGAGGCCT AAAAATATAA TTTAAAAATA CATTGCGTAT TTTCTAAAAC      60
AATAAATTTA TAGTGTTAAT ATTCATAGGG TCAATCAAAA TGAAGCTTCT CCTTTGGGCC      120
TGCATTGTAT GTGTTGCTTT TGCAAGGAAG AGACGGTTCC CCTTCATTGG TGAGGATGAC      180
AATGACGATG GTCACCCACT TCATCCATCT CTGAATATTC CTTATGGCAT ACGGAATTTA      240
CCACCTCCTC TTTATTATCG CCCAGTGAAT ACAGTCCCCA GTTACCCTGG GAATACTTAC      300
ACTGACACAG GGTACCTTC GTATCCCTGG ATTCTAACTT CTCCTGGATT CCCCTATGTC      360
TATCACATCC GTGGTTTTC CTTAGTACT CAGTTGAATG TTCCTCCTCT CCCTCCTAGG      420
GGTTTCCCGT TTGTCCCTCC TAATCTCGAG                                450

```

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

```

GAATTCGGCC AAAGAGGCCT ATCAGGTGAT TTAATAATAA TTTAAACTA CTATAGAAAC      60
TGCAGAGCAA AGGAAGTGGC TTAATGATCC TGAAGGGATT TCTTCTGATG GTAGCTTTTG      120
TATTATCAAG TAAGATTCTA TTTTCAGTTG TGTGTAAGCA AGTTTTTTT TAGTGTAGGA      180
GAAATACTTT TCCATGTGTT AACTGCAAAA CAAGATGTTA AGGTATGCTT CAAAAATTTT      240
GTAAATTGTT TATTTTAAAC TTATCTGTTT GTAAATTGTA ACTGATTAAG AATTGTGATA      300
GTTTCACTTG AATGTCTCTT AGAGGGTGGG CTTTGTGTTA TGAGGGAGGG GAAACTTTT      360
TTTTTCTAT AGACTTTTTT CAGATAACAT CTTCTGAGTC ATAACCAGCC TGGCAGTATG      420
ATGGCCTAGA TGCAGAGAAA ACAGCTCCTT GGTGAATTGA TAAGTAAAGG CAGAAAAGAT      480
TATATGTCAT ACCTCCATTG GGGAAATAAGC ATAACCCTGA GATTCTTACT ACTGATGAGA      540
ACATTATCTG CATATGCCAA AAAAATTTTA AGCAAATGAA AGCTACCAAT TTAAAGTTAC      600
GGAATCACCT CGAG                                614

```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```

GCGAAGACCA TCAAATGAAT TGTCACAATA CTCGAATAAT GCAAGACACA GAAAAGGATG      60
ATAACAATAA TGACGAATAT GACAATTACG ATGAACTGGT GGCCAAGTCA TTGTTAAACC      120
TCGGCAAAAT CGCTGAGGAT GCAGCCTACC GGGCCAGGAC TGAGTCAGAA ATGAACAGCA      180
ATACCTCCAA TAGTCTGGAA GACGATAGTG ACAAAAACGA AAACCTGGGT CGGAAAAGTG      240
AGTTGAGTTT AGACTTAGAC AGTGATGTTG TTAGAGAAAC AGTGGGGCTC GAG              293

```

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

```

GAATTCGGCC TTCATGCTTA CTCAGAAAGC CACTGCCCCA AACAAGCCAC CTGCATTATC      60
AAACACAGAG AAGAGGAATC ATTCCGCCTT TTGGGGACCA GAGAGTCAAA TCATTCCTGT      120
GATGCCAGAT AGTAGTTCCT CAGGGAAGAA CAGAAAAGAG GAAAGTTATA TATTTGAGTC      180
AAAGGGTGAT GGAGGAGGAG GGGAAACACC AGCCCCAGAA ACAGGTGCAG TGCTACCCCT      240
GGCGCTGGGT TTGGCTATCA CTGCTCTGCT GCTTCTCATG GTTGCATGCC GACTACGACT      300
GGTGATCCTC GAG              313

```

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

GCCCATTCCG GCCCCATCT CACCCAAGAT CCCCAGAGT CCAGGAGCTG GACGGGGACA      60
CCCTCAGCCC TCATAACAGA TTCCAAGGAG AGGGCACCCT CTTGTCCTTA TCTTTGCCCC      120
TTGTGTCTGT CTCACACACA TCTGCTCCTC AGCACGTCGG TGTGGGGAGG GGATTGCTCC      180
TTAAACCCCA GGTGGCTGAC CCTCCCCACC CAGTCCAGGA CATTTTAGGA AAAAAAAAT      240
GAAATGTGGG GGGCTTCTCA TCTCCCCAAG ATCCTCTTCC GTTCAGCCAG ATGTTTCTCTG      300
TATAAATGTT TGGATCTGCC TGTATTATTT GGTGGGTGGT CTTTCCTCCC TCCCCTACCA      360
CCCGTCCTCG AG              372

```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GGAGCTAAAT TTAAGAAATG CAACTAGCCA GGTGCTAAGA AGCTCAGTTA CACGTTTCTC 60
 AAAAGTTGGC TGTTAGTTCC ATGACTCAGA GTGCACTCAA ATCATTTTAA TTAICTGAG 119

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GAATTCGGCC TTCATGGCCT AGGTCCTGTT TGCCTATTTG AGCTGCTATT AGTGTGAGAA 60
 GAAACTCAGA TGATAGTAGC AGAAACAGAA AGAGGAAGAG GCTACAAGAG ATGGTAGATG 120
 CTGAACTTAA GGCATTTGAT AACCAATGGA TATAGAAAGA AAAGGAAATG AAAGGACAAA 180
 AATGGCTCTA AGTTTTCAAA CTTGACTGAT GAGGAAAATA TTCACATCAA GAATGGACTG 240
 AAGAAATAAG GAGGAGATGC TGGGTTAGGG TGAAAGGAGA TGAGCCCAT TTTACATTGG 300
 AAAGCTCTAT GGAACAACGG AAGTAGTAGT AGCTTTATAT TCCAGTATGC CAAATTCTCA 360
 GCTCCAAGAC TCCAGCACTG TGTGCTCTAC AGTATGTTTT GTGATGTGCC TGAGTTTGG 420
 TTTCTTTATT TCAATTAGGG ACTCTTCATA CCAGGGTCAG GGGTTATGCT CGAG 474

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GAATTCGGCC TTCATGGCCT AGTTCCTGTG CTCTTGAAAG AACAAAGTTGA TGCTTGTA 60
 GCTGTTTGA TTATTTT TAG GCGCATGATA ATGGAGCTTA CAATGAATAA AAAGACATGG 120
 GAACAGATGT TGCAAACTACT ACTCAGGATA ACAGAAGCTG TCATGCAGAA GCCAAAGGAT 180
 AAACAAATAA AGGACTTGTT TGCCCAGAGC TTGGCAGGGT TACTATTTAG GACGCTCATG 240
 GTAGCTTGA TCCGAGCAAA CCTCTGTGTG TACATTTCTC GAG 283

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GAATTCGGCA CGAGGGGCGG CCGTTTTTTT TTTTTTTTTT TTTTCAGGTG CACATAAAGT 60
 TAGTTTATTA ATGACTATAT TTTGAAGCCA GCCATTTTGT CCAATATTTA AATAACAAGC 120
 TGTTTAATAT TAAAGCAGAA AGTACTGCCA CATTGTGACA GAAGTACAGC TTTATCCATA 180
 AACCCCTTAC ACAATTATAC ATTAAATGCT ATTTTTATTT AAGCAAGGCA CCCCTACTTG 240
 TTCTAAAATA TGGGATGTAC TACACCATGT ATTACTCGAG 280

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

GAATTCGGCC AAAGAGGCCG GAATTGGGCC CTCGAAACCA AGAATTCGGC ACGAGGGAAT      60
GAAATTAGCT AACAGCCTTC AGCTACAGAA ACTTTGGGAT CCAGACAGCA TTTGAGCTGA      120
CGCCACGCCC TTCTCAGGCA GCGCCACAG TGAAGGAGSA GGATCTAGAA GGGCCCGGCC      180
ATTTTTCCTC AATGTAGGGT CCCTCTGATG GGAATTCTTT GTCTGGAGAC CCGAGCTGAG      240
ACTTTGTCAG ATTGGCATCT CTGTCCCTGC TCAATGCTGC TTCCATGCT CCCTTTTCTA      300
TCACAGACAT CATAGCCTGA AATCTTTCCA CACCCAATAC TGCTTCCTAT ACCCCTTAGC      360
CTTTCCTGAT CTCATTGAGG TTACCATTTT TCCTCCGTCG CTCGAG                      406

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

GAATTCGGCC AAAGAGGCCG GAATTGGGCC CTCGAAGCCA AGAATTCGGC ACGAGGCTTT      60
TTTAGGTAAT TCTTTGTACT CCTGCTGTCT ACCTCTCCTC ACACCCAGC ACCCCCATT      120
TTTTCAAACC TTGGTATCTG TTGGGTGAAC AGTATAATCT TTTCATCTGC TTTTAGAATG      180
TGGGATATTT CCAGTACCTA CTTTTTTTTT TTTTITTTGC TGAATCCAAA GATATATAAA      240
TAAAAATAT ATATTTTATA AAGATCAGAA TGATATAAAG GAGATACATG TTTCTTCCTT      300
TAAAAAATAA ACGGAAGTTA CATTGTTAAT GTTCATATTA TGATGCGAAT TCTCTGGTTC      360
CTCCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

GAATTCGGCC TTCATGGCCT AGGATGTCTG AGGTCTTAAC CTGCCAGTC CTGAATTCCT      60
GGGACTTCAA CGACTCTCTC TCTGCCAAT GATGTGAGTC TTTAGGTAGA GTTATAGCGC      120
AAAGGGCTAC TATCAATGTT ATTAAGCATA AATTATGACT AGAGCCACAG AATGATTTCC      180
TCATTAATCC AAAAAAAAAA AAAAAGCAAA CCACTCTTTT ACTTTATGAT GAGCACATAA      240
ACAGTTTTT TTTCTTTTA TTTATCTACT TTTACTTACT TAAATTTTAG AGATGGGGTC      300
TTGCTATGTT GCCCAGACTA GACTCAAACCT CCTGGGCTCA AGTGATCCTC TAGCCTCAGC      360
CTCCCAAGTA GCTGGGACTA CAGGAAGGAG CTACTGCACC TGACTCAATT TTTTTTTTTT      420

```

CTGAGATGGA GTCTCACTCT GTGACCCAGG CTTGTCTCGA G

461

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GAATTCGGCC TTCATGGCCT ACATCAATAA CAGCCAAACT GAGACACATA ATGTTTTCTA	60
CGTCCAAGAG GCTAAATGTG AGAATCCAGA ATTTGAGAGA AATGTGGAGA ATACATCTTG	120
TTTCATGGTC CCTGGTGTTC TTCCTGATAC TTTGAACACA GTCAGAATAA GAGTCAAAAC	180
AAATAAGTTA TGCTATGAGG ATGACAACT CTGGAGTAAT TGGAGCCAAG AAATGAGTAT	240
AGGTAAGAAG CGCAATTCCA CACTCTACAT AACCATGTTA CTCATTGTTC CAGTCATCGT	300
CGCAGGTGCA ATCATAGTAC TCCTGCTTTA CCTAAAAAGG CTCAGATTA TTATATTCCC	360
TCCAATTCCT GATCCTGGCA AGAATCTCGA G	391

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

GAATTCGGCC TTCATGGCCT ACGTGAAGAC AAGATGAAGT TCACAATTGT CTTTGCTGGA	60
CTTCTTGAG TCTTTCTAGC TCCTGCCCTA GCTAACTATA ATATCAACGT CAATGATGAC	120
AACAACAATG CTGGAAGTGG GCAGCACTCA GTGAGTGTCA ACAATGAACA CAATGTGGCC	180
AATGTTGACA ATAACAACGG ATGGGACTCC TGGAAATCCA TCTGGGATTA TGGAAATGGC	240
TTTGCTGCAA CCAGACTCTT TCAAAAGAAG ACATGCATTG TGCACAAAT GAGCAAGGAA	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GAATTCAAGG CCACGCCGGA GCTGTACCTT GGAAGGAGGA GCCAAAAATT ATGCTGAGAG	60
TGATCACAGT GAAGACGAGG ACAATGACAA CAATAGCCCC ACCGCAGAGG AGTCCACGAA	120
GAAGAATAAG AAGAAACCAC CGAAAAAAA GTCTCGTTAT GAAANGACAG ATACCGGTGA	180
GATAACATCC TACATCACTG AAGATGATGT GGTCTACAGA CCAGGAGACT GTGTGTATAT	240
CGAGAGTCGG AGGCCAACA CACCGTATTT CATCTGTAGC ATTCAAGACT TCAAATGGT	300
AAGCGTTTTT AATGTGCTGT TCACTCTGCT CTGTATTCTC TCTTTTCCA GTTCCATTGG	360

CGCTCTCGAG

370

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GAATTCGGCC TTCATGGCCT AAAAACCTTA CAACTAAAGC AAATAGACTT TTCAAGAATT	60
TAAATAGGAT TCCTTCCCTT TAATCAATTA ATTATCCACT TTGTCATGGT GTCAACCTGT	120
AATTTTCATGG TTTTGTGTGT GTGTGTGTGT GTGACAGAAA TTTACAAACA ATGTGATCTC	180
GAG	183

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GAATTCGGCC TTCATGGCCT ACAACTAATT TGATCATATT AACAAGAGGT TGGTTTTTAA	60
ACCAAGCAGT ATAAATATAA ATACAGCCTT GGGTAGATCA TAGTCAAAC ATCCAAATGC	120
AACCTCAGCT TCAAAGATTG TAAAGTCTTT TCTTCCCTT CCTTTTTTTT	180
TCCTCCAAAT ATTTATTTAC TACCTACCAT GTGCCAGGCA CTGTGATGGG CTATGAGGAT	240
GCAGTGGGG ATAGGACAGA TGCCATCCCT GCCCTGAGGA GACTTGCAGT TTATTGGAAA	300
AGATGGACAT CGTAAATAT ACAATCATAC AAATAAAAT TACATAAATA ATTCAGTACT	360
TCAACTTGTG GGAGGTACAG CAGTTTATAA TAATAACATC CCTCCCACCT TCTTGAGAGA	420
GTCATTGGTT GCCCCACTTC TCTTCATGAA TGAGAGGACA TGATTAAACC TATCATTTCA	480
GGTAGGAGTT TACTGTGGGA TGGATATCAA TCTTCTATTA ATATGTTTGT GCTCATGCTC	540
TCCATTTTGC AATGGACGTC TCGAG	565

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GAATTCGGCC TTCATGGCCT AAAATGAAAG CTATGTCTTA GAACCAATGA AAAGTGCAAC	60
CAACAGATAC AAACCTTCC CAGCGAAGAA GCTGAAAAGC GTCCGGGGAT CATGTGGATC	120
ACATCACAAC ACACCAACC TCGCTGCAAA GAATGTGTTT CCACCACCCT CTCAGACATG	180
GGCAAGAAGG CATAAAGAG AGACCCTCAA GGCAACTAAG TATGTGGAGC TGGTGATCGT	240
GGCAGACAAC CGAGAGTTTC AGAGGCAAGG AAAAGATCTG GAAAAAGTCT CGAG	294

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

```

GAATTCGGCC TTCATGGCCT AGCTTCTGGT AATGGCGGAC TAGATGATTT AGAGCAACCC      60
ACCCATTGAA AAGAACTACA AAACGTCAGA TCTCTAAAAG GCTACAAAAT TAATACAATT      120
GTGAGGAATT GCTAGGTTAT ACTACAAGAG AACAGAAGCA TCCAGAGAGG TAAGCCTAGG      180
ACTTAAACT ATATTTTAT TGAAGGTATC TGTGGTTGAG TAATAAGCCT GTGCTAAACT      240
GCGTGGAAT TATGGCACAT TCAAGGCACT ATAGTAACAG AAGTCAGAGC CCAAGGCCCA      300
TCAAAGGGG TGGAGTGTTC CTGACAAAC CATCACCCAT AGTATGCTGG GAACCGCAAA      360
TGTTTATACC TTCAGGTAA TTGTAATCAA AAAATATACT AGCCCTTACA AAGTCTTGTA      420
GCTTGGCTTT GCATCATCTG GGTGGACTAG TGAAGTGTAA GTTCTGAACA AATATTATGG      480
AGGCAACTCG AG

```

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

```

GAATTCGGCC TTCATGGCCT ACTTCCCTGA GCTGGGGTTT CCCTGCTTGT CCAAGTTGTGA      60
GCTGTCCTCG GTGTTACCGA GGCTGTGCCT AGAGAGTGGA GATTTTGTAT GAAAGGTGTG      120
CTCGCTCTCT GCGTTCATC TTCTCTCTCC TCCTTGTTCC TGCAAACCAC AAGATAAAGG      180
TAGTGGTGTG TCTCGACCCC ATCAGCCTCT CACCCACTCC CAGACACACA CAAGTCCTCA      240
AAAGTTTCAG CTCGTTGTGT GAGATGTGCA GGTTTTTCT AGGGGGTAGG GGGAGACTAA      300
AATCGAATAT AACTTAAAT GAAAGTATAC TTTTATAAT TTTTCTTTT AAAACTTGGT      360
GAAATTATT CAGATACATA TTTAGTGTC AAGGCAGATT AGTTATTAG CCACCAAAAA      420
AAAGTATTGT GTACAATTG GGGCCTCAAA TTGACTCTG CCTCAAAAAA AAGAAATATA      480
TCCTATGCAT CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

```

GAATTCGGCC TTCATGGCCT ACAAAATTGA TTATGACAAG ATTGTCTACT ATGAAGCAGG      60
GATTATTCTA TGCTGTGTCC TGGGCTGCT GTTTATTATT CTGATGCCTC TGGTGGGGTA      120
TTTCTTTTGT ATGTGTGCTT GCTGTAACAA ATGTGGTGA GAAATGCACC AGCGACAGAA      180

```

GGAAATGGG	CCCTTCTGA	GGAAATGCTT	TGCAATCTCC	CTGTTGGTGA	TTTGTATAAT	240
AATAAGCATT	GGCATCTTCT	ATGGTTTTGT	GGCAAATCAC	CAGGTAAGAA	CCCGGATCAA	300
AAGGAGTCGG	AAACTGGCAG	ATAGCAATT	CAAGGACTTG	CGAACTCTCT	TGAATGAAAC	360
TCCAGAGCAA	ATCAAATATA	TATTGGCCCA	GTACAACACT	ACCAAGCTCG	AG	412

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GAATTCGGCC	TTCATGGCCT	AGTTAGGTGG	CTTTTAGTGT	ATTGACAAAG	TTGTGAACCC	60
ATTATCACAA	TCTAATTTTA	GAACATTTTT	ATCAGCCTCC	TTGCCCCCTA	AAAAAACCCA	120
GTACTTTT	CCAATCCAST	CATTTAAAC	TTACTACATA	TTTAATAGAT	GGATAGATAG	180
ACAGGAGGAT	GGACAGACTG	AAGGAAGAAT	GGATGATTAT	GTATAAATA	ATGAAAAAAC	240
AAAACTATC	CCCAAATCAT	AAGGGTATAC	GCAATGCTTT	CCTGTGGCAA	AAGATTCGGA	300
ACATGTACAG	CAGATTTTTT	TTCAAATGTT	CATAATTCTA	AATTCCCAAA	ATGGTCTACA	360
CAACTTCTCG	AG					372

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GAATTCGGCC	TTCATGGCCT	AGGAGAAAGG	AAGGGAAGCA	TTACTGGGTT	ACTATGCACT	60
TGCGACTGAT	TTCTTGGCTT	TTTATCATT	TGAACTTTAT	GGAATACATC	GGCAGCCAAA	120
ACGCCCTCCC	GGGAAGGCGC	CAGCGAAGAA	TGCATCCTAA	CGTTAGTCAA	GGCTGCCAAG	180
GAGGCTGTGC	AACATGCTCA	GATTACAATG	GATGTTTGTC	ATGTAAGCCC	AGACTATTTT	240
TTGCTCTGGA	AAGAATTGGC	ATGAAGCAGA	TTGGAGTATG	TCTCTCTTCA	TGTCCAAGTG	300
GATATTATGG	AACTCGATAT	CCAGATATAA	ATAAGTGTAC	AAAATGCAAA	GCTGACTGTG	360
ATACCTGTTT	CAACAAAAAT	TTCTGCACAA	AATGTAAAAG	TGGATTTTAC	TTACACCTTG	420
GAAAGTGCCT	TGACAATTGC	CCAGAAGGGT	TGGAAGCCAA	CAACCATACT	ATGGAGTGTG	480
TCAGTATTGT	GCACTGTGAG	GTCACTGAAT	GGAATCCTTG	GAGTCCATGC	ACGAAGAAGG	540
GAAAAACATG	TGGCTTCAAA	AGAGGGGATC	TCGAG			575

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

```

GAATTCGGCC TTCATGGCCT AACAGGGTCT TGCTCTGTCA CCCGGGATGG AGTGTAGTGG      60
CGCAATCACA GCTCACTGCA GACTCAGCCT CCCAGGATCA AGCAATTCTC CCACCTCAGC      120
CTCCCAAGTA GCTGGGACCA CAGGTGCACA CCATCATGCC CAGCTAATTT TTGTATTTT      180
TTGTAAAGAC AGGTTTCACT GTGTTACCCA GGCTGATCTC GAACTCCCGT ACTCAAGCAA      240
CTCCCCACCT CAGCCTCCCA AASTGCTGGG ATTACAGACG TGAGCCACAG CCGCGGGCCC      300
CAAAATCTAT TTAAATGTA AAGAAACCCA AAAGTAACAG TTTTGTAAAA GAAAATTCAC      360
GTACTGTTT GTAGTAAATT CTAACACTG TGTATCTTTG TGTCTAGTTA AATCCTAGGC      420
TTACAGCTAA AATTCATGA GAAGGCAAGT ACTCGAG                                457

```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

```

GAATTCGGCC TTCATGGCCT AGAAAGCTAT CATTATTGA GAGTTAATTG TATATTAAGT      60
ACCATGCTAA GTGCTTTGTA TGTATTATTT ATCTTTATAA AAATCCTATG AAATGAATAC      120
TGTTATTTTC CCCCATATA CAGATGAAGA TAGAGAAAGG AAGAAAAGGG AGGGAAGAG      180
GAATACCATT TCACTGAGCA ATTTTACTGA AATATTTTAT GGAGCATTG TGGGTTTGT      240
TTGTTTGCTT GTTTGTTT TTTGTTTGT TTTTTTTGT AGACAGAGTC TCACTTTGTC      300
GCCCAGGCTG GATCTCGAG                                319

```

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

```

ACGGTGAAAC CCTGTCTGTA CTAAAAATAC AAAAAATTAG CGGGGCATGG TGGTGGGCAA      60
CTGTAGTCCC AGCTACTCGG GAGGCTGAGG CAGGAGAATG GCATGAACCC AGGAGGCGGA      120
GCTTGCACTG AGCCGAGATC ACGTCACTAC ACTCCAGCCT GGGCGACAGA GCGAGACTCC      180
GTCTCAAAAA AAGAAAAAAC CAAGACAAAA CAAAAAATAA CTTTGTCTGT TAAGTACAAT      240
ATCTGTGTTT CTCAGGGACA GTTCTATTG ACCATTGTTT TTCTTGTC TAAGTATCC      300
TTTCCTTTT TTGTACATCT TGTAATTTT GTTTTATTAA AACTGGAATT TTAATAATAA      360
TGCAGTGTGG CAACTCTACT GCTTGATTTG GCTCAAAGGT ATATTATTTA TTTTAAATA      420
TAACAAACCA ATATTGGGT TCTCTATTCT ATAGTTTGTAG CATTTTGAAT GCAACAACTG      480
TCTTATTCAC CATTTAATTC TCAGTACTAC CGTTTCTAGT ACACAATATG CACTTAATGA      540
ATATGAGGGT CCTCGAG                                557

```

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

```

GAATTCGGCC TTCATGGCCT AGACCGTGCC AGGTATTGAG ASCGACCCTC ACATTCCTAC      60
AGTGCTCTGT GTGGCATCTT AATGAAACTT TATTCTCTCC CCTTAAATGA GAAAGAATAG      120
CTAGTTGTCA TCCTTTCTGA ACCGATTTTG TCTTCAAAG GTAGTAGTGT ACCAGGCGCTG      180
CTATTTTGCA AAACGGTCTC CACCAAAATC GAATTACCTG CCTCGCGGGG CAGGCGTGTT      240
GACCAGGTGG ACTCTAGAAG TAGGTGGTTT GCTTGGTTTC TTTTCCTTTT AAGGTTTCCC      300
TTTCTTCTTC TTCTTTCTG TGTTTTTTTT TTTTTTTTTT TTTTTCATAT ATAGAAACTG      360
TCCCTAAGAG AGGAAACCTT TCTGGCCATG TTATTCCAGG AATCTTTTGT CCCCTAAGTT      420
TGACCTTGTT CTTTCGTTCA CCCTTTACTC TTGCATCTCG AG                                462

```

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

```

GAATTCGGCC TTCATGGCCT ACATAAAATC AGTTGACTAT TGTGCAACAT AGAATTATTG      60
TTTGTGTGAA ATTACCGCTG AAGGACCTTG CCTACATTCA AGGGTCTATT TTTATTTTTC      120
CAGGTATTCT TTCACATTAG TGACATTATA GTCTAGTACA ACTGCTTGAT AATTGGGAGA      180
AACTAACATT AATTTTAGAT AGTGATTGAT AAAATTTGGC CTGCCAAATG CATTTTAAAA      240
ATAATTCTAG GATTTATCTA TGCTCATTTC TAGTATACCT CATGATATAT AAGACATCTT      300
TCTTTTGTCA TATCAGTTCT TCAGATACTA AGACAGAGGT CCTCGAG                                347

```

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

```

GAATTCGGCC TTCATGGCCT AGGTGGTGCA ATAATTATAA ATGTTGCCAG TCAATGCCAA      60
CCAGTGTCTG ATTGGCTTCC TGTGCATGTC CAATTTCTCT TGTGACACTG TGTGGTGCC      120
AGAGCTTCTG AATCTTCTTG AATCGCTCTT TGCATAAATG TAAAGGATTT CCCCGTCTGA      180
GTCCCTGGTC GGTCTCCCA TAATCATCAA GGTAAGGAGG AGAATAAAAA CAGCCTTTGG      240
TTTGGCCAGC TAAAAATAGC ACCTGACATT CCCGTACTCT CAGGAAGATG CCCACTCCAG      300
AGCCACAGGA GTAGGTGTGA GCTGTGCAGG CTCCTACATC CTCCCTTCC AGTTCAGTCT      360
GGCAGCAGTA ACTCTGGGAG CACAGCAGAG ATCCGCACAC AAGGCACAGA GTTGGGGCTC      420
TGCTCTTATC ACCACCTGAT TTGGGGCACC TCGAG                                455

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

```

GCATGAAGGC CCGCCTTCAT GGCCTACAGG CTATGTACTG TATGATTCCA AATATGACAT    60
TCTGGAAGAG GCAAAACCAG GGACACAGTG AAAAGATCAG GGGTTGAGAG GGGAAAAAAG    120
GAGGGATGAG TAATCAGAAC ATACAAGATT TTTTAAAGGC AGTGGAAACCG CTCTGTATAA    180
TACCATAATA GTGGATACGT GTCATTATGC ATTCATCCAA ACTCCTAGAA TGTACAGCAC    240
AAATAGTGAA CTGTAATGTA AATGCAGTGT GTAGGTGTTT ATACAAAAAA ACAGATGGAA    300
AGATTTTGTA CATAGCTCTA TGTGAAAATG TATTTATTTA TTAAGAGCAA AAATATGCTT    360
ATTTCAAATT TCCACGTACG ACTTTTTCAT AAAGACACGA TCCACTGAAA TAACCTCCCA    420
AAAGAATTTC TATAATCTAT AGCAGGTGTA CATGTTGTTA ATCAAGTGCT TAATGTTACT    480
CGAG                                                                    484

```

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

```

GAATTCGGCC TTCATGGCCT ACCCCACCAG AGGACAGACG TTGAAAGATA CCACGTCCAG    60
TTCTTCAGCA GACTCAACTA TCATGGACAT TCAGGTCCCG ACACGAGCCC CAGATGCAGT    120
CTACACAGAA CTCCAGCCCA CCTCTCCAAC CCAACCTGG CCTGTGATG AACACCACA    180
ACCCAGACC CAGACCCAGC AACTGGAAGG AACGGATGGG CCTCTAGTGA CAGATCCAGA    240
GACACACAAG AGCACCAAAG CAGCTCATCC CACTGATGAC ACCACGACGC TCTCTGAGAG    300
ACCATCCCCA AGCACAGACG TCCAGACAGA CCCCAGACC CTCAAGCCAT CTGGTTTTC    360
TGAGGATGAC CCCTTCTTCT ATGATGAACA CACCCTCCGG AAACGGGGGC TGTGGTCCG    420
AGCTGTGCTG TTCATCACAG GCATCATCAT CCTCACCAGT GGCAAGTGCA GGCAGCAGTC    480
TCTCGAG                                                                    487

```

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

```

GAATTCGGCC TTCATGGCCT AATTTTATTT AAATTTTAT ATTTATATAT TTTATTTAAA    60
ATTTTCATGA AATGGCCAAG CAGGGTTTAA TATAAAATGG AAACAGGGTT TATCTCAGAA    120
ATTTGGTGGC TAAATTCCTT GTATCCCGTC TTATCTAGGG ATGTTGTTTG TTTCAAGGTT    180
CTACCTTGAG AGGAGCTGT CATTTTCTTT TTTGTGTGCT GCTTTGCCTA GTTGACATCT    240
TGGCTTTATG TGCTCCTGTT GAATGCATTG GGAAATTTTC TTTCTTCTTT CTATGTCCTG    300
AAATAGCTTA TATAAGAGGG AAATCTCGA G                                                                    331

```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

```
GAATTCGGCC TTCATGGCCT AAAAAATAC TTTCATTGT TTTGCTATTA CTAGTTTCTC      60
ATTTTTTATT GCACTTGCAA TCATTTTAGG AATATCCTCA AAATATGCTC CAGATGAAAA      120
TTGCCCAGAT CAAAATCCTC GTCTCAGGAA TTGGGATCCA GGACAAGATT CTGCAAAGCA      180
AGTTGTTATC AAGGAGGGGG ATATGCTCCG TCTGACCTCA GACGCCACCG TGCATTCTAT      240
AGTCATTGAG GATGGAGGAC TGCTTGATTT TGGGGACAAT AAAGATGGAT CCAGAAATAT      300
TACTTTGAGG ACTCATTACA TCCTGATCCA GGATGGTGGG GCGCTTCATA TTGGAGCAGA      360
AAAATGCCGC TATAAATCCA AAGCGACAAT TACCTTGTAT GGCAAGTCAG ATGAAGGTGA      420
AAGTATGCCA ACATTGGGCA AAAAGTTTAT TGGTGTGGAA GCTGGCGGGA CACTGGAGTT      480
ACATGGGGCA CGGAAGGCAT CGTGGACGTT GTTGGCAAGG ACCCTGAATT CCTCAGGCTT      540
GCCGTTTGGG TCCTATACCT TTGAAAAGGA CTTTCCCGG GGCCTCAATG TGAGGGTCAT      600
TGACCAAGAC ACGGACGCTC TCGAG
```

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

```
GAATTCGGCC TTCATGGCCT AGAGAACTTT TTGAGGGCTT TTTTTTTCC CCTTTTAAGC      60
TATTTTGTAT GTAGACTTAA TTTTCTAAT TTTGCCACTT CTGGCAATCT GAAATCATTG      120
AAAAGGACAC AATTCAAATT TATGTTAAAG GTCATAAATT TTGCCCAGGA CTCAATATTT      180
TCTCATTTTT CCAAAAATAA AATCTTATTT ATGCATTATA GCGACTTGGT TTTCACITTA      240
TCTTGAATTA TAGCTTTTAA GAGGCAGAAA GAATCCTTTT TATAAGGACA GTCTCAAGTG      300
TACACACAGA TTAAATATTA CAAATATAGG TTGCAATAA AACTTTCAAA ATGTGGGATT      360
ATAGGAAGCA AAAGAGAACC AACCAAAGCA TCAACAAATT TACCTTTTGT TTTTTTTTAA      420
AGATTTTCT TATTTCTTA GCTGCTTTG CATTAGCATT AAATAACATT CTTATTGGAG      480
TGGTATGTGC ATGGCCCAAG CTCGAG
```

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

```
GAATTCGGCC TTCATGGCCT ACTCCAGCTT TATTATCTCA GCTACCATCA AACTATATTA      60
CATCAAATTA TCATCATTAC TCTCCTGCAC AGTAACTTTC TTTCTGCTCC ACTAAGAAGC      120
TTACTCCCAT CCTGTTTATT CTCTATATCG TAGCTGGACT AATCTTTTCA AAGTGCAAAG      180
CCAATCACAA TACCACCTGC TTAATAATCCA TCAGTGGCTA ACTTTTCATT CTAGGACGAA      240
AAGAAAATTC TATAACATGA CTTCAAAGGC TCTGCATGTC CTTCTATTTT TCTGTCTCTC      300
```

TCTAGTCTTT TCTTTGATGG TCTCCACTCC AGCCCTACTG GCTTCTTTCT GGAATCAATG 360
TCACCCACAA CCCGTCACGC CACTCGAG 393

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GAATTCGGCC TTCATGGCCT ACTCCGCTCT GGCCAGAGG GAGGCCAAGA AGGACGAGCC 60
CAAGAGCGGC GAGGAGCGGC TCATCATCCC CCCCGACGCC GTCGCGGTGG ACTGCAAGGA 120
CCCAGATGAT GTGGTACCAG TTGGCCAAAG AAGAGCCTGG TGTGGTGCA TGTGCTTTGG 180
ACTAGCATT ATGCTTGCAG GTGTTATTCT AGGAGGAGCA TACTGTACA AATATTTTGC 240
ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT 300
AAATGAGCCC TCTGCAGATG CCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA 360
AATCTTTGAA GAAGAAGAGC TCGAG 385

(2) INFORMATION FOR SEQ ID NO:641:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GAATTCGGCC TTCATGGCCT AGCAAGGAGA ACTATTGTCT TATGATCAGC TTGCCATCT 60
TTCTGTCTCT TATCATGTTG GTGGAGGTGG CCGCAGCCAT TGCTGGCTAT GTGTTTAGAG 120
ATAAGGTGAT GTCAGAGTTT AATAACAACT TCCGGCAGCA GATGGAGAAT TACCCGAAAA 180
ACAACCACAC TGCTTCGATC CTGGACAGGA TGCAGGCAGA TTTTAAGTGC TGTGGGGCTG 240
CTAACTACAC AGATTGGGAG AAAATCCCTT CCATGTGCGA GAACCGAGTC CCCGACTCCT 300
GCTGCATTAA TGTTACTGTG GGCTGTGGGA TTAATTTCAA CGAGAAGGCG ATCCATAAGG 360
AGGGCTGTGT GGAGAAGATT GGGGGGCTCG AG 392

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GAGTTGAAGT GGCCAAAAAA TTATAACACT CTCCTACTTT CATATCTTGA TTTTAATTTT 60
TTCCCTTACT TGTATTTTAT TTCTGAGTGG CTAATGGATC TTAGTCTAAG AACTGGAGGT 120
GGAGAACTCG AG 132

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

```
GCACAAAGAC GCATTCATC TGAGTTTCCC TGAAAGCTAG AATAAGTTTG CTGGTGTCAG      60
CTGGGATCCT GTCTTCTATA GCTTTGTATC AAGCAAATC AGCATTGTGT CTTGAATGCA      120
TGTCATGTGC AGCCTGCGTT TATGTGCGAC TGAGCACTTG GGTGGGGACA TCTTAAGGCT      180
GTTTATATTT CTTTTTCATG TGTGTTGTT GTTGTGTTG TTGTTGTTTT GGAGAGAGTC      240
TCGCCCAAAG CTCGAG                                     256
```

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

```
GTGCTCGCAG CCNTGGTGGC CTGGCGCTCG GCGTNCCTTG TCTGCCTCGC TTTCTCCTTG      60
GCCACCCTGG TCCAGCGAGG ATCTGGGGAC TTTGATGATT TTAACCTGGA GGATGCAGTG      120
AAAGAACTT CCTCAGTAAA GCAGCCATGG GACCACACCA CCACCACCAC AACCAATAGG      180
CCAGGAACCA CCAGAGCTCC GGCAAAACCT CCAGGTAGTG GATTGGACTT GGCTGATGCT      240
TTGGATGATC AAGATGATGG CCGCAGGAAA CCGGTATAG GAGGAAGAGA GAGATGGAAC      300
CATGTAACCA CCACGACCAA GAGGCCAGTA ACCACCAGAG CTCCAGCAAA TACTTTAGGA      360
AATGATTTTG ACTTGGCTGA TGCCCTGGAT GATCGAAATG ATCGAGATGA TGGCCGCAGG      420
AAACCAATTG CTGGAGGATG GCTCGAG                                     447
```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

```
GCTCAGCAAC ATTTTAGGAA CAACATTGGT GAGTATATGA GAATAGCCGT GACCTCCATA      60
TTTCATCAGC CGGGTTTTCG TATGTATGTC ATGTGCTACC AGAATTCGAT CTTACAGGCC      120
CTCTTCCACC AGGAGACGCA CCCTGTGAAA AATGTAACT CATTAGATGT CATTGTCTT      180
TCATTTTCGC TTTTCAGGAT GCTTTCAACT TTTTACTCAT TAACCTATG TGCTGTGCT      240
AAAGATACTG ACTTCTACTG TGGCGTGTGT ACTGAGAGAC TCGAG                                     285
```

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

```

GGAGATTGA AGAAGAATTG AATGAAAGGA TGATTCAAGC AATTGATGGG ATTAATGCAC      60
AGAAGCAATG GCTCAAGTCT GAAGACATTC AGAGAATCTC ACTGCTTTTC TATAACAAAG      120
TACTAGAAAA AGAGTACCGG GCCACGGCAC TGCCAGCGTT CAAGTATTAT GTGACTTGTG      180
CCTGTCTCAT ATTCTTCTGC ATCTTCATTG TGCAGATTCT CGTGCTGCCA AAAACGTCTG      240
TCCCGGGCTA TCTCGAG                                         257

```

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

```

GGGGCAGCAG TAAAATCCAG GCCCGAATGG AACAGCAGCC CACTCGTCCT CCACAGACGT      60
CACAGCCACC ACCACCTCCA CCACCTATGC CATTGAGAGC TCCAACGAAG CCTCCAGTTG      120
GACCCAAAAC TTCTCCCTTG AAAGATAACC CGTCACCTGA ACCTCAGTTG GATGACATCA      180
AAAGAGAGCT GAGGGCTGAA GTTGACATTA TTGAACAAAT GAGCAGCAGC AGTGGGAGCA      240
GCTCTTCAGA CTCTGAGAGC TCTTCGGGAA GTGATGACGA TAGCTCCAGA CTCGAG      296

```

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

```

GTGCANATGT ACGGTGACCA CCTGGCCCTT GACCGGGCGG CTCGAACCTG GCGGCCCTGG      60
GACCAGCGTC TTCTTCCTCA ACAGCCCGTT CCCCAGAATG TCCAGCCACT CTTCTGGGGC      120
CGGGGCTGGG GCGGGCTCGG GCTCCATGGC AGCAAGGAAC TCTCGGGCCA GGGCCCCAGG      180
CTGCTCANCC TCCTCCGCCG GGGGTGTGCC CATGTCCTCC AGCGGTGGCA GCTCACTCAG      240
GTCATCCTCT TCCTCCTCTT CCTCCTCCTC TTCCTCCTCA CCCTCTGCAT CCTCAACCCC      300
ATCCAGTACC TCGAAGTCCT CGAG                                         324

```

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

```

GAATTCGGCC TTCATGGCCT ACTTCCTGAT ACAGATACAT TTACTACAGA AAATTCCTT      60
TATAGGTGTA AATTTCTGTT TACAACAGGC GAGTCGAAAA ATAATAAGAA CAAAAGGAAA      120
AAAAGCAGTC ATACTTTATT TTAGGCAGTT GAGGGGTAGC TGAATAAGTT ATCCTGTGTT      180
GTTTGGTTCT GTTACTTATA GCTCAAAGTC ATCAATATGC CAGGGTGGCA TGTTCGGGA      240
TGGTGCAATC TTGTCTTTG CAGTCATTTA TCAGGGTGGC GTTCCTAAA TTCTAACACA      300
GACCTCGAG                                     309

```

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

```

GGTGACGCCT GCTTCACATC TCTAATGAAC ACCCTCATGA CGTCGCTACC AGCACTAGTG      60
CAGCAACAGG GAAGGCTGCT TCTGGCTGCT AATGTGGCCA CCCTGGGGCT CCTCATGGCC      120
CGGCTCCTTA GCACCTCTCC AGCTCTTCAG GGAACACCAG CATCCCGAGG GTTCTTCGCA      180
GCTGCCATCC TCTTCCTATC ACAGTCCAC GTGGCGCGGG CCACCCCGGG CTCAGACCAG      240
GCAGTGCTAG CCCTGTCCCC TGAGTATGAG GGCATCTGGG CCGACCTGCA GGAGCTCTGG      300
TTCCTCGAG                                     309

```

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

```

GCAAGGGCAG GCGGGTCCCC CAGTCCCGCC ATTACGGGTT GTCAGACCGT CTGCGTGTGG      60
CAGGGCTCCC AAGGGCAGGC GGGTCCCCCA GTCCCGCCAT TACGGGTTGT CAGACCGTCT      120
GCGTGTGGCA TTTTGTGGCT TATAAGCTTC ACCCACTCAC CCCCAACCCA CACCCACAT      180
CCCCCTGCCG GCAGCCCCTC AACCTAAGAA GGCCAGAGCA TATTTATTTT CGGAGGGAGC      240
AGATTACTTC TCCCAGAGAA AGGAAAATCT TGGAAAAGAT TAAAAACAC AAATCTAAGC      300
CTTGACGGTT TTTTGTCCC TTTTGACCCC CTTCCCATCT CTTCAGAATT TATCCCATG      360
GCTTTTTTTT TTCTGTGCG TGTTCGAG                                     390

```

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GAATTCGGCC	TTCATGGCCT	ACCAAATTCC	CTGCCTGTGC	CTGCTGGGAC	CAGACTCCGC	60
TGTCATGAGG	GTGACATCCG	CCACCTGTGC	TCTTCTGCTG	GCTCTGATCT	GCAGCGTCCA	120
GCTGGGGGAT	GCCTGCCTGG	ATATCGATAA	ACTGCTTGCG	AATGTTGTGT	TTGATGTGTC	180
CCAAGACCTC	CTGAAGGAGG	AGCTTGCTCG	TTACAACCCC	AGTCCCCCTG	CAGAGGAGTC	240
CTTCCTCAAT	GTCCAGCAAT	GCTTTGCCAA	TGTCCTCGAG			280

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GGTGTTTGGC	CACAGTTCGG	GACCTATGGT	AGAAAAATAC	TCAGTAGCTA	CCCAGATTGT	60
AATGGGTGGC	GTTACTGGCT	GGTGTGCAGG	ATTTCTGTTC	CAGAAAGTTG	GAAAACCTGC	120
AGCAACTGCA	GTAGGTGGTG	GCTTTCTTCT	TCTTCAGATT	GCTAGTCATA	GTGGCTATGT	180
GCAGATTGAC	TGGAAGAGAG	TTGAAAAGA	TGTAAATAAA	GCAAAAAGAC	AGATTAAGAA	240
ACGAGCTCTC	GAG					253

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGGCCTCCC	AAAGTGCTGG	60
GATTACAGGG	GTGAGCCACC	GCACCCAGCC	TGTGAAATAC	TATTTTATG	GTAAGCTAGA	120
ATTTTAAAC	TATTTCTTGC	AAGTTTAGGA	TTAAATGAAT	TACATTATGT	AAAATTACAT	180
CTTTGTCTGT	ATTACGTATT	TGTATACAGT	TGAATAGTTT	TGGTAACACG	TACCTTAGTG	240
CTTTACATTG	ATTGGCTCAT	TAATTTTATA	TTTTGAGTAA	TAATCATCTA	ATTTTATTAT	300
TGTACAATTC	AGTCTTAAAT	TATGTTATGA	TGTGAAAATG	GTAGCTTTCT	TGAGTGTTAT	360
TATTTTGTG	GTAGTGGGCA	ATGTAATTAT	CACACATAAA	ATGAACTGTG	AGACTTTTGA	420
GCCTGAAATA	TTATTCATAT	TATAATGCTC	CTCGAG			456

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

```

GAATTCGGCC TTCATGGCCT AGTATATACA TGCATTTAAT TGTGATTTTA TCACCTTTCC      60
CATTTCCTTC CCCACAAGCT GGCATTTTCAG TAGTTGCTTT TGAATAATGG TTTTGTTAC      120
CTGGGAAGGC AGGCCCAGAA CCCATTTCTT TGAATTGCAG TTCCGGGCTG TGTTCACATG      180
ACTGCTGTCT AGCTGATGCA TTTTTCACAT TTSTCAACTC TGGTTAGAAA CAGGTCCTCA      240
GGAGTATTCT CTAACCTGAT ATTTTCTAAA AAGATATGTT GATTCAACTT TGTTTAGCAT      300
CCTACTTTCT AGATTGTGGG GCTCATTTCG CCAGGGCCAA GCTACCAGAA AAGTAGAAGT      360
GGAGATTACC TGGTATGTAT CTCTCTGGGT GCCCCAGTTA GAGCTGCCAC AGCTCAGGAA      420
AAAGATGAGG CATAACGACC TTGAATGTAA TTGGAGTAAG TGACAAAATA AGAACTACCC      480
TGGGAAACTC GAG                                         493

```

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

```

GAATTCGGCC TTCATGGCCT ACTTGGCCTT TGTTTGTGTT TGCCTTTGTC AGTCTCCTGC      60
CTCTGGATGG GTTTCGTGTT GTTTCCAAAC TGTCTGGGCG TGTGCACCAT GGAGACAGTG      120
TCCTGGGCTG CCTCTAGCCT GATCTGGTTA GAATAAGCCC CTCTCCTTTG CATGCGTCTC      180
CAACCTGACA TTTGGAGCAT CCAAACAAA TCATGACATT CCAAGTAAA GATAGAAACC      240
ACCGTCTCCA CTCCACTCGA G                                         261

```

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

```

GAATTCGGCC TTCATGGCCT AGATGGTCTC TGCTGCTCTT GCCTCTAGTT CATGGAGATG      60
TGCTCTGTGTT CAGGCCAAGA TACAGCCAGC CAGGCCTGTC GTCTGGGACC CAGGAGGCCT      120
CTGATGACCA AGGGCTTTCA CATCCTAAGT CATTTGGAAG GAGGCCTTGA GAACAAAGTC      180
ACCTTTGTCA CTCCAGTGA ACTGAATGAG GAACATGCTG TCTCCTGTCT TGGCCTCCCC      240
TTTCATGAGA TACTGGGGAG AAGAGAACAT TCCTCCTGGC TTAGTTGTAG CAGACCCAGA      300
CCTGTGCCCA GCTTTGGTCC CCCTTCCCAA CTTCGTAAGC ACGTGCTGCA GAGCCACCTT      360
GGTCTGAGCA CCTGAGGACC AGCCCCCTCT CCCTCAGTGC GGGTCATCTC TTGGGGGATT      420
TTCTTAAAGT GAAGAAAGGG GGTGGGAAC CATATTGCCC CTCCTCCCC CATCAAACCTT      480
CCTTCATTTA ACTTGCTATA AAATGAGTCA TATAAAGAAA CTCTATATGG GTGAGGTATA      540
TCCCACCTCT GTGAAAACAT TACAAATCAA ACCGCTTCTC TCAGTTTATT TAAGATGCTT      600
TTGTTGCAAG CGGTACTCGA G                                         621

```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

```
GAAGTCTTGG AGATTCTAG TTTATTCATT AACAGCAGAA GGATGGAAGA AAATTCCTCT    60
GGCAATACCA TGTCAGCCTC TTCGATGTTT AATACAGAAG AAAGAAAATG TTTGCAGACT    120
CACAGAGTCA CGGTGCATGG GGTCCCAGGG CCAGAGCCCT TTACCGTTTT CACTATTAAT    180
GGAGGCACCA AGGCAAAGCA GCTTCTGCAG CAAATTCTGA CAAATGAACA AGACATCAAA    240
CCTGTTACCA CAGACTATTT TTTGATGGAA GAAAAATATT TTATATCTAA AGAAAAGAAT    300
GAATGTAGGA AACAAACCATT CCAGAGAGCC ATTGGTCCAG AAGAGGAGAT CATGCAAATT    360
TTAAGCAGCT GGTTCACAGA AGAGGGATAC ATGGGCAGGA TTGTCTTAAA AACCCAGCAG    420
GAAAACCTAG AAGAGAAAAA CATGTGTTCAA GATGACAAAG AGGTGATCTT GAGCTCAGAG    480
GAGGAGAGTT TCTTTGTCCA AGTGCATGAT GTTCTCCAG AGCAACCTCG AACAGTCATC    540
AAAGCACCCC GCGCCAGCAC ACTCGAG                                     567
```

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

```
GAATTCGGCC TTCATGGCCT AGGCCCTTTG GCCCTGGGGT GGGGGTGCTT ACTACATCCC    60
TGGAAGGTGC AGGGAGGCTG ATGGCCTTGA TCTCTAACAC AAACAGGAAC CAGCTTCCTC    120
CCTCCCCCAC CCTGGGTTCC CAGGGCCTCC GGGTGTGAGA TCCTCCCCCA CTGCAGTGCC    180
CCACCCGCTC CCCACAGAAG CCCGAGAGT GGCTCTGTCA CCAGAGGTGT CATTTCCAG    240
CTGTCTGTGG GAGGTGAGTG AGCAGGGAAT GTGTGTGCTG GGTGTGGGAA CTCAGCCCAA    300
TCTAAGAGAA GATACTCTTG GCTTCCTCCC CCTCAGAGGA GCAGCCGCGT CCCTGGTCTT    360
TGTGCACTGA CAGTCCCGGA GTCTCGAG                                     388
```

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

```
GAATTCGGCC TTCATGGCCT AGCCAGGAGT TGAGGTGGAA GTCACCATTG CAGATGCTTA    60
AGTCAACTAT TTTAATAAAT TGATGACCAG TTGTAACTT CTGTTGGTTT TTATTCAGAA    120
TACTGGCAGA TTTTAGGAAT ATAAAGGTGT ACTATGAGAC TTCCACTTTT CAGGTGGAAT    180
ATATGGGTAT CTTAGAGTGG TCTATCCTGT TTTCGTTGTC GTTTGAGTCA TTTGAAAAC    240
GGATTCCGTT AACTACATAA TATGTGAGAC CTGACTGGTT TTATTGGACA CTGGCAGTTT    300
ATAACTTTGG CATACTCTAG ATAAATCTG ATTGGTATGG GGTGTTAAGG TTTCTGGGCG    360
GTTTGTAATG CACACCCATG GTTGAGAACC TAGTGCCTA GTAGGCACGT GTTAAAAAGC    420
TAGTAACTAA TATTTTAAAA TTAACCAAGT TTAACGTCCT TAAAAAAGGA TTAAGTGGCA    480
AGGACCTCGA G                                     491
```

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

```

GAATTCGGCC TTCATGGCCT ACCTCAATAT GCTATCAGAT TCTGAAAATT CCCAGCATCT      60
GGAAC TTCAT GAGCCACCAA AAGCTGTGGA TAAGGCGAAA TCCCAGGGG TTGATCCTAA      120
GCAGTTGGCA GCAGAACTCC AGAAGGTTTC ACTACAGCAG TCACCGCTGG TTCTGTCATC      180
AGTTGTTGAA AAAGGATCTC ATGTTTCATTC AGGTCTTACA TCAGCAGGAT CCAGTCCGCT      240
TCCCAGCCCT GGGCAACCAG GGTCCCCTC AGTGAGCAA AAGAAGCACG GCAGCAGCAA      300
GCCACTCGAG                                     310

```

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

```

GAATTCCTAT GGCCTACTTC CGGCGCAAGT GGCTTCTGAT AATCATGGCG CCCCTCGGAA      60
CAACTGTAT GCTGTGGAGC CTCTTGAGGA GTTCTCCGGG CGTGGAACGG GTCTGTTTCC      120
GGGCTCGAAT CCAGCCCTGG CACGGTGGCC TGCTCCAACC GCTACCTTGC TCTTTCGAGA      180
TGGGGCTGCC ACGCCGCCGG TTCAGCTCCG AGGCCGCAGA ATCTGGTAGC CCAGAGACCA      240
AGAAACCTAC ATTTATGGAT GAGGAAGTTC AAAGCATACT CACGAAAATG ACAGGCTTGA      300
ACTTGCAGAA GACTTTTAAG CCAGCTATAC AAGAACTGAA GCCACCAACC TATAAGCTAA      360
TGACTCAGGC ACAGTTGGAA GAGGCTACAA TACAGGCTCT CGAG                                     404

```

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

```

GAATTCGGCC TTCATGCCTA ATTTGTGTGA TGGCCAAAGA GTTCTTATCA GAAGTGGCAA      60
AAACTACATA CAGGTTGGCT TCCAATAACA TGAGCCAGGT ATTTTTCAGT AATATTTTGA      120
AGTGTCTTTT CTTTCTAGAC ATGCACATGA TGGTGTCCTA GCCAGAACAG TGGGTAAAGC      180
CAATGGCTGT AGCAGGAGCC AATCAGTACA CCTTTCATCT CGAG                                     224

```

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

```
GAATTCGGCC TTCATGGCCT AGGTCTACCA AAGTGAGGAC ATTACTGCAG ATATTCTTCT    60
CCTTTTCTCC TACATTATCA TTCTCTTTT ATAACATCAT TTCTGCAGAT ATGTAAAAAT    120
ACATCCCATC TTCAAAAAGA AAAACAAAAA TCTGACTGTA CTTTCATATCC CCTTCTAGAC    180
ATTGCCACAT TTCTCTACTT CTGTTTACAA CAAAACCTCT GGAAAGATTT GTCTATACTG    240
GCTTTCTCTA CTTCTTTTAC TTCCATTCCCT TTCCTAACCA CTCTAAACAT GCTTGGGTCC    300
CCACCACTGT AACAAATATA ATTGTGTCC AATAACCAGT GATCTCTGTA TCACCGGTTT    360
CAAGGGTGAG ATCTCAGACT TCACCTTTCT GGATTGATTG ACACATTGGA CTCAGTTGGT    420
TACTCTCAC TTCTGAAAC TGTCTTCACT GGGCTTTTGG GACTCCATAT CTCGAG    476
```

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

```
GAATTCGGCC TTCATGGCCT ACTCTCTACT CCTTGTGCT CAATTTCCAT TGTGGAATTC    60
TGCATATATG ATCTTGTGGC ACATTTCTAC ATTTCCTCAG CCCAGAAGGC CTTCCCTGTT    120
CACTATCTCC TTCTTTTAC TAACCTTAC TATATTTCCA GGCACAGTTC AGGCATCAGA    180
TAGCCCTATT TGTTCAACT TTCACCGTAG GTCAGATTAT AAGCCTTGCA ATCTCGAG    238
```

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

```
GAATTCGGCC TTCATGGCCT AGACCATTTT CATTGTTTAT AGTTTATTTT TTATAAATAG    60
TGCTTTCTGG AATATCCTTA AATACCTCTA TCTTTTAAAC ATCCTTGTGT ATACATCTTT    120
TCTCACACTT GGCTTCCTCT TGAATAGAA TCTCCTGGAA ATTAGATAGC TGAGGTAAAA    180
GTCCCTGAAC CTTTACAAA TTGCTACACA ATAAATACCA AACTGATTTT CAGGAATGTA    240
GTCCCATCAA CAGTGTGCTT GTTTATCCAT ATCGTTGCTG ATCTGAGTTT TGTCAGTCTA    300
TTGATTCTTA CCAATCTGCC AGTATCATAG ATTTTAAAT ATTTTGTG TGTCATCTCGA    360
G
```

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GAATTCGGCC	TTCATGGCCT	ACTCATACAC	AATGAATACA	AAAACCTGGAA	CTCTGCAATT	60
TAATACTGTT	TCCAAACTGG	ACACTGGAGA	ATATTCTGT	GAAGCCCGCA	ATTCTGTTGG	120
ATATCGCAGG	TGTCTGGGA	AACGAATGCA	AGTAGATGAT	CTCAACATAA	GTGGCATCAT	180
AGCAGCCGTA	GTAAGTGTGG	CCTTAGTGAT	TTCCGTTTGT	GGCCTTGGTG	TATGCTATGC	240
TCAGAGGAAA	GGCTACTTTT	CAAAAGAAAC	CTCCTTCCAG	AAGAGTAATT	CTTCATCTAA	300
AGCCACGACA	ATGAGTGAAA	ATGATTTCAA	GCACACCCTC	GAG		343

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCGGCC	TTATCCTACA	ACTTTGAATA	GACATAAGAG	TGCCTGTCTG	CATAAACCTT	60
CATCAACATT	GGTATTATCT	TTCTTTTTCA	TCTTTGTAA	TTGGATAAGT	TTTAAAAAGT	120
GTAACACATT	TTAGTTTGCA	TAGCTTTGAT	TATAAGTGAG	GTTCGACATT	TTTTTTCATT	180
TCTTTACACT	TTAAAAAATC	TAACCGTGGC	AACGTTTGCA	GGTGTGTGTT	CTTCTTATGT	240
TGCTGAGTGT	TATTTACTCC	TGGACG				266

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GAATTCGGCT	TCATGGCCTA	CAAAAAAGAA	ATTAAGAAGC	TCCTAAAGAC	GCAAAGAAAT	60
CATCTACTCC	TCTGTCTGAA	GCAAAAAAAC	CAGCTGCTTT	AAAACCAAAA	GTACCCAAGA	120
AGGAAGAGTC	TGTCAAGAAA	GATTCTGTTG	CTGCCGAAA	GCCAAAGGAG	AAGGGGAAAA	180
TAAAAGTCAT	TAAGAAGGAA	GGCAAGGCCG	CAGAGGCTGT	CGCTGCAGCT	GTGCGCACTG	240
GAGCCACCAC	AGCAGCTGTC	ATGGCGGCAG	CTGGAATAGC	AGCCATTGGC	CCTGCCAAAG	300
AACTCGAAGC	TGAGAGGTCC	CTTATGTCAT	CTCCTGAGGA	TCTAACCAAG	GACTTTGAAG	360
AGTTAAAGGC	TGAAGAGGTC	GATGTAAACA	AGGACATCAA	GCCTCAGCTG	GAGCTAATCG	420
AAGACGAAGA	GAAACTGAAG	GAAAACTCG	AG			452

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: dcuble
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

GAATAATTGA CTGAAAGTGT AGTGTGCGAGT GGTAGAATAA GTGCTGATCC TGGGGTCTTA	60
TACCAATGTT GCTAACTGTG AGCAGCCTTT GTCAAATCAC TTGGCTTCAT TTTCAGTGGC	120
CTAAGAGTAA TAGGTTTAAT TATTTCCATA ATTCCCTTAA GTTTTTACAT TTTCTGAGTT	180
CATCTTTTGT GTTTTTCCTG GCATTTTACT ATTCCTCTTT CCTGCTTTTG GCTATTTTCT	240
CAACAGGTCC ACGACTGGAA TTTGAAAGCA AGAAACATCT CGAG	284

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GAATTCTGGA AGCAGCCTAT CATCGCTCCG TCTGCCCTCC ATACACAGCG TTTGTGTGTG	60
TTATGCCAAA CTGCTTGGTG TTTTCCAACC GTGGACCATG ATATCTCACT TCCTTAACCT	120
TACCTTCATA TGCTTTTCCT TTGTGTCTTC TTCTGAAATG CTTCTTCCTT TTGTCCAGGC	180
TGACTCCTGT TTGTCTGAGA CATGTGTCTC AGGAAGCCTT TCCGTTCCCC TCGAG	235

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GAATTCGGCC TTCATGGCCT AGCATTGATG GCCCATGTAG AAGACCTCAT CATTAAAGACT	60
ATAATCTCTG CTGAACTAGC TATTGCTACT GCCTGTAAAA CCTTTGTGCC TCATCGCAGC	120
AGTTGTTTTG AACTCTATGG CTTTGACGTG CTCATAGATT CTAATCTGAA GCCATGTTG	180
TTGGAAGTGA ATCTCTCTCC TTCTTTGGCC TGTGATGCGC CTCTGGACCT AAAGATTAAA	240
GCCAGTATGA TTTCAGATAT GTTCACTGTT GTAGGATTTG TGTGCCAAGA TCCTGCCCAG	300
CGGGCATCAA CTCGGCCAAT TTATCCCACC TTTGAGTCTT CCAGGCGAAA CCCTTTCCAG	360
AAACCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GAATTCGGCC	TTCATGGCCT	ACACAGACAT	CATCATGCAG	AAGATGACCA	TTTCCAACAT	60
GGAGGCAGAT	ATGAATAGAC	TCCTCAAGCA	ACGGGAGGAA	CTCACAAAAA	GACGAGAGAA	120
ACTTTCAAAA	AGAAGGGAGA	AGATASTCAA	GGAGAATGGA	GAGGGAGATA	AAAATGTGGC	180
TAATATCAAT	GAAGAGATGG	AGTCACTGAC	TGCTAATATC	GATTACATCA	ATGACAGTAT	240
TTCTGATTGT	CAGGCCAACA	TAATGCAGAT	GGAAGAAGCA	AAGGAAGTAC	TCGAG	295

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GAATTCGGCT	TCATGGCCTA	CCTGCCTCGA	GTGATGGGTA	TCGGGATGGG	TATCGGGATG	60
GCCACGCGG	GGATATGGAT	CGATATGGTG	GCCGGGATCG	CTATGATGAC	CGAGGCAGCA	120
GAGACTATGA	TAGAGGCTAT	GACTCCAGA	CTCGAG			156

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GAATTCGGCC	TTCATGGCCT	AATAATTTGT	AAGTTAAAAT	AAGTAATACA	AATTAAATGC	60
AAATCAAATG	CCTGAAGAAG	AAGCACGAAT	ACCTATTTTG	AAATCTGCTG	TAGCCGAGAC	120
AGCTTCTAAA	TCTCCCACTT	GGTTCTGTT	TCTGGAAGGT	GTGGGTCCTG	TGGTAGCTGG	180
AGTGTGGTG	GCCATCTTGG	TGCTGGCGGT	CCTCATGCTG	ATGTACTACT	GCTGCAGACA	240
GAACAACAAA	CTTGGCCAAC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAATTCTGGA	TCAAACAGA	GGAAAATGGT	GGGAATTCTT	GTATAGATAC	AGTCTAACAT	60
AGAAACCCAT	GCCCATCAGC	AGTAATTTCC	AGTCCCCCAG	TCCTCCAAGC	CCTGGTACTC	120
GAG						123

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

```

GAATTCAGAG ATAAAGCTAA AGTTCATTG GAGCACCAGC CCAAATCCTG GACTTCTTTC      60
TGCTCCTCCT CAGAGGTTCT CTGGTTATAA GTTTTATGTG TATCTTGCCA GAATTTTTC      120
TATGTTATTA ATACAAATAT ATGTAGCCAC AGAAATTATA GCGTGTCAAT CAGCCTTTGG      180
TTTTATTGTC ATTGATAGTA TTATGTCCAT ATCACTCTAC AACTTCTTAG GCCATGAAGG      240
CCG                                     243

```

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

```

GCGATTGAAT TCTAGACCTG CCTCGAGACC ACCTATGGAA GCCAAGTGT CCCGGGCCAT      60
GAGACCTGCC CAATCAAGCA GAAACACATT TGGAGAGACA AACAAACACG ACACGCTCGA      120
G                                     121

```

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

```

GAATCTAGA CCTGCCTCGA GTACCTGATC TTTTACTGTC TCTATAGGTT CATCTTTTTC      60
TTCCCTTTGT TAATTCTACT TTTTAGTTTT TTTGCTAGAT TTTCTTGCA ATTGGATAGG      120
CCCATTTAAC CTATTTTGCC TCCACTCTAA ATTCAGTACT CCAAGAATTG GTTTCACTCT      180
TCCAAATTTT GTATATAAGC CAGAGTTCTG CATAAAGGAA AATACTTAAA TTCTTTCTAA      240
TCTAATGTGG TTTCTGTCAT CTTTCAGGAA ACTTTTCCTC GAG                          283

```

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

```

GAATTCGGCC TTCATGGCCT AGGGTTTGTG GCTAAAAATT ATGCTTAAGA ACACATCTAA      60
CAAACCTAAA GCTGCAAAGA CATAATGTTA ATGTAGGTGA AAATTTCACT TGTGTTTATT      120
CTGATAGACA AAATTGTATT TTAGATGAGA AGCAACAATT TTCATGTTGT ACTGAGATTG      180
TTAGTAATGA AATACTTCCA AATATTAGTG ATGGTAGAAA TCTAGTGTAG GGCTCTTTGC      240
TGAGAAGGGA AAAAAGTCAC ATAAGAAATC TACTTTTCAG TAAACTGCAA ATATGTGTGC      300
TTCAACCTAT AACATATTCT GTCACTTTGA GCTTGTCTATA TTGACAGAGA ATGAAAACCT      360
GATAAGACTC GAG                                     373

```

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

```

GAATTCGGCC TTCATGGCCT AGAGCGACTT CGACACCATG CCAGACATTG AGAGTGATAA      60
AAACATCATC CGGACCAAGA TGTTCTTTTA CCTGTCAGAT TTGTCCAGGA AGGACCGGAG      120
AATTGTCAGC AAAAAATATA AAATTTATTT TTGGAACATC ATCACCATTG CTGTGTTTTA      180
CGCGCTGCCC GTGATCCAGC TGGTCATTAC CTATCAGACA GTAAGTGCTA AACCTAGCCC      240
CAAACCCCTC GAG                                     253

```

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

```

GAATTCGGCC TTCATGGCCT AATCGAGGAG AATGGAGACC AAACCTGTGA TAACCTGTCT      60
CAAACCCCTC CTCATCATCT ACTCCTTCGT CTTCTGGATC ACTGGGGTGA TCCTGCTGGC      120
TGTTGGAGTC TGGGGCAAAC TTA CTCTGGG CACCTATATC TCCCTTATTG CCGAGAATC      180
CACAAATGCT CCCTATGTGC TCATCGGAAC TGGCACCCTT ATTGTGTCTT TTGGCCTGTT      240
TGGATGCTTT GCTACATGTC GTGGTAGCCC ATGGATGCTG AAACCTGTATG CCATGTTTTCT      300
GTCCCTGGTG TTCCTGGCTG AGCTCGTAGC TGGCATTTC A GGGTTTGTGT TTCGTCATGA      360
GATCAAGGAC ACCTTCCTGA GGA CTTACAC GGACGCTATG CAGACTTACA ATGGCAATGA      420
TGAGAGAATG CTCGAG                                     436

```

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

```
GAATTCGGCC TTCATGGCCT AGTCCCCACT TTATCTCTTT AAACGGTTTC TTTTCTTTT    60
TTTTTTTTTA GACCTCTCAG GGATGAAACA TTTTATTTT TAACTAGTT TTTTCTTTT    120
ATAACATTAA CACATGCTGA ATGCTTAAAT CTTTCTAGAA TTCAGAAAGG TAAATGAAA    180
GTCACCATTC TCATTCTCAT CATCTTACTC CCAGAGATGA TTGTTATTAA TATTCCAGA    240
AATTTTGCTT GTATATGCAA ACAGCAATAT ATTGTAGCTG CTCGAG                286
```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

```
GAATTCGGCC TTCATGGCCT ACCCTTACCA GATACTGAAT CTGCCAGTGC CTTATTTTGG    60
ACTTCTCAGC CTCCTGGGCT GGGTGAGGTG GTTCACTACC AGCCTTGGCA CCATAGTGAG    120
ACTCCCATCT CTACAAAAA AAAAAAAAAA AAACCTTCTG TTGTTTGTA GCTACCCAGT    180
TTATGGTATT TTGTACAGC AACCCAAACA GTCTGAGACG TTTAGCTTAA CTCCTGTATG    240
CACTAGATAC AGTCTGCACT TTGACATCAA TCTCGA                276
```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

```
GAATTCGGCC TTCATGGCCT ACTAAGAATA GGAAAAAAAA TAACACTATG ATACCACAAC    60
CTTATTACAT CAAACTGCTT TGGGCTTTAT CCTCTTTAAA GTGTGCTCAG GTGTTCAAGC    120
ACGAGGTTTC TGACAGCCCT CATAAGACCT TCGAG                155
```

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

```
GAATTCGGCC TTCATGGCCT ACTTTGAAGA GTACGATTTT AAAACCAGCA ATTGGTGTGA    60
ATGCAAAAAC ATTTGTTGGC ACCATTATT TAAAAA AAAAGCTGTA TGCAGCAGAA    120
```

```

AGCCTTATAC AAGTTGTTTT TCTTTTTTTC CTTTTTCTTT TTTTGGGTAC CTTCAATTTCT 180
GTTACTTTTA TATAAAATTC TCTGCAAAGG AAGGCCTCTC TTTGGACTAC AATTTGGAGG 240
CAGCCACTTG TTGTGCCTGC TTCTGTAAAA GAATGTGGAT ATCAAGCCCC CCCGACTCGA 300
G 301

```

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

```

GAATTCGGCC TTCATGGCCT AATTTTTTACA GAAATTATTT CCACAATCAG AAGTACTGTA 60
CTGATTGCAT TTCTTTGTCT CAAAAAGTTT TCCTTATGTT TCTCAAAGCA GTATTTACAC 120
TAATTATTCA ATTCTTATCT TTCTTTCAGT TTCTCCAAT AGACTGTGAG ATCTTTGAGG 180
GCCAGGTTGA CATGTCTCTG ATACCTACAC CCTATGCAGC TCCTAGTGCA GGACCTTGCA 240
GTGACAAGCT CGAG 254

```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

```

GAATTCGGCC TTCATGGCCT AATATTTATT TAGATGCTAT TATTACTGTT TGGACTTTTA 60
TTTTGGCAGG CTTTGTTCCT GACTGTAGGG TTTTCCAATG TGACTAATGA CCACTCCTGC 120
CTCTCCCGTG GTGTATTTTG GGCACCCTCC CACCCGGCTG CATACCCGGC CAGGGCTCCC 180
ACAGAGACAA GGAGGGCACA GGTGTCTGCC CCCTCTTTGA AATCGATATA CACACATCCA 240
CGCACATGCG GCCCACTCGA G 261

```

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

```

GAATTCTAGA CCTGCCTCGA GCTTCTGGCT GTTGTCTTTG CTGGGCATCC TTTTACAAG 60
TGGAAGAACT AGGATGGCTT TCCAAAGTCT TCTAGAAATG AAGTTCTTTC TCTGTGCAGC 120
TTTCCCCCTT GGAGCAGGAG TGAAGATGTT TCATTATCTT GGGCCTGGGA AACCACCTCC 180
CCAGGCTTCT CCCTCCCCCC ACCCCCGACT CGAG 214

```

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

```

GAATTCGGCC TTCATGCCTA CAAACTTAAA AGTAAATCTT TGGAAATCAG ATAGTAGTCT      60
TGAAACTATG GAAAACACAG GAGTGATGGA TAAGGTTTCAG GCAGAGTCTG ATGGGGACAT      120
GTCTTCAGAT AATGACTCAT ACCACTCTGA TGAATTCCTT ACAAATTCTA AGTCTGATGA      180
AGACAGGCAG CTAGCTAACT CATTAGAGAG TGTAGGGCCA ATAGATTACG TTCTTCCTAG      240
TTGTGGTATT ATTGCCTCAG CGCCTCGATT GGGCAGTCGG TCCAGTCTC TTAGCAGCAC      300
ACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

```

GAATTCGGCC TTCATGCCTT ACTCCATATT TATTAGATG CTATTATTAC TGTTCGACT      60
TTTATTTTGG CAGGCTTTTT TCCAGACTCT AGGGTTTTCC AATGTGACTA ATGACCACAC      120
CTGCCTCTCC CGTCGTCTCT TCTGGGCACC CTCCACCCG GCTGCATACC CGGCCAGGGC      180
TCCCACAGAG ACAAGGAGGG CACAGGTGTC TGCCCCCTCT TAAAATCGA TCTACACACA      240
TCCACGCACA TCGGACCCCG AGGAAACGAA ACCCACTCTA GAAAACGCGA CCTTGGCCGC      300
ACCTAAAGCA GCCAGCCGTG AGTGCAGACC CCTTGGCCAG CGTGGCGCAG TGCCCTGAG      360
CAGTAGTGGC GTGTGTGTAG ATCAAGTCGG ATCTAGTCCA GCTCGGTTCA TTAGCGATCC      420
ATGTAATCTG ACGTCATCTT GTCTCGAAGT CTCTTTTTTT GGCCAGGCC TTGAAGAATA      480
CACTGGACTC GAG

```

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

```

GAATTCTAGA CCTGCCCCTG CCTCTGCAT CCAGCCCCCA ACATGGTGCC AAAGCTTCCA      60
GAAGCCAAAA AGCTTCTGAT TTITAAGGTA GTGGGCATCT CTCTCCTAAT GACGAAGCTG      120
CTCAGCAACT CCACCTGCCC GCCGAGGAA GGAGCAGTCC CCTGCTATCC CTGCAGCCAC      180
TCCCAGCACA CCCGACACCA GCCAGACCA CCGCCCACTC TCGAG

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```
GAATTCGGCC TTCATGGCCT ACTGGCTCAT ACAATACATC AATAAGTATG CAACTTTTCA      60
TTTGGTATTT CGTTGCTGGA AGTGGGAAAT ACCCCATCTT CCCAGGAGTG AAATGTTTCT      120
ACTTTCTCTC CGTGGTGCCC TGTATCATTG CTCAGCTCTG CTGCTGCTCT CCGCAGCCCC      180
TAAAAGTAGC ATGGATCGGG GAAGAAGGAA GGACGGCAGG AAGGCAGGCA GAGATCCTCA      240
GGCAGGTCGA G                                     251
```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

```
GAATTCGGCC TTCATGGCCT AGTGTGTGTG TCGGTGTGTG TGTGTTTACA TATAAAGTTT      60
TTTGGTAACA AATAAATTTT GTTAGAGCTA GTCAGATTTT TGTGCTTGA ATCTGCTAGT      120
TTTGGTAGGT TATATTTTTC AAGGAATTTG TCCATTTTCA CTATGTTGTT GAATTTTGGG      180
TGTAACGTTT TTCATTACTC TTTTCTTTT AATATCTGTG GGATCTGTAA TGATGCCCCC      240
TCTTTCATTC CTGATATGAG TAATCTTAT TCTCTTTTGT TCTATCAGCT CGAG          294
```

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

```
GAATTGGCCT TCATGGCCTA ATTGGGACCA AATAGAGGCT CACAGATATT TGGATTATTT      60
TATGTGCTTA TTATTAAATA AGGAAAGCAT TTTGTGATAT GTGGAAGACG CTATGTGAAG      120
TTTTACCTAT CTTCTCAAAG ACCTTTTCTT TTGTATTTTC TTTTGGTGTT TCITAAAGCC      180
AAACAAAGAA ATGTTCTTAA GGAGACAGGG TGGGTTTTTC TGTGGGCCTA GGCCATGAAG      240
GTCGAG                                     246
```

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

```
GAATTCGGCC TTCATGGCCT ACCCTAATAT AAAAAGCATT GTCACCATGT TGATGCTGAT      60
GCTATTGATG ATGTTTGCTG TCCACTGTAC CTGGGTCACA AGCAATGCCT ACTCTAGTCC      120
AAGTGTTAGTC CTGGCCTCAT ACAATCATGA TGGCACCAGG AATATCTTAG ATGATTTTAG      180
AGAAGCTTAC TTTTGGCTAA GGCAAAATAC AGATGAACAT GCACGAGTAA TGTCTTGGTG      240
GGATTATGGC TATCAGATAG CTGGAATGGC TAATAGAACT ACGTTGGTGG ATAATAACAC      300
CTGGAATAAC AGCCACATAG CACTGGTGGG AAAAGCTATG TCTCTCGAG      349
```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```
GAATTAAATA AGTTACTGAC TTTGTGACTT ATTTAATTCA TATTAATATA TTAGGCTTCC      60
CAACTGACGG TGTTCAGATT GAGCTAGCTT CCAGTTTTGG AGAAACACAT AGTTGATTAG      120
TTCTGTCACT AATTTTCAGG GATATTAATA TAACTTTGAT ATTAGTGAGA AATTTTCTTT      180
CAGTAGTAAA ATGTTTTCTA ACTTAGGAGC TGTTCTCGAG      220
```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

```
GAATTCGGCC AAAGAGGCCT AGCAGAGCTT TCATATCCAC GATGCGTTTT CTGGCCGCCA      60
CGATCCTGCT GCTGGCGCTG GTCGCTGCCA GCCAGGCCGA GCCCCTGCAC TTCAAGGACT      120
GCGGCTCTAA GGTGGGAGTT ATAAAGGAGG TGAATGTGAG CCCATGTCCC ACCGATCCCT      180
GTCAGCTGCA CAAAGGCCAG TCCTACAGTG TCAACATCAC CTTTACCAGC GGCACCTCAGT      240
CCCAGAACAG CACGGCCTTG GTCCACGGCA TCCTGGAAGG GATCGGGGTC CCCTTCCCTA      300
TTCCTGAGCC TGACGGTTGT AAGAGTGGAA TCAACTGCCC CAGTACAGTC GAG      353
```

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GCGATTGAAT TCTAGACCTG CCTCGCTTCC CCACCCTTAC TAACATTAAC GAAAATAACC	50
CCACCCTACT AAACCCCAT T AAACGCCTGG CAGCCGGAAG CCTATTGCA GGATTCTCA	120
TTACTAACA CATTTCCCC GCATCCCCCT TCCAAACAAC AATCCCCCTC TACCTAAAC	180
TCACAGCCCT CGCTGTCACT TTCCTAGGAC TTCTAACAGC CCTAGACCTC AACTACCTAA	240
CCAACAACT TAAAATAAAA TCCCCACTAT GCACATTTTA TTTCCCAAC TCCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTCGGCC TTCATGCTTA GCCTCAGCTC TTTCTTCTGG GTTGTGTTGTA TTTCTTTTC	60
TGTCCCAAAC AGTTTCCCC ACAAAAAGAA CTTTATGTCT TTCTCTGTCT TCCCTCAGTC	120
CTTCCAGTCA GCAGCCTGTG ATTGGGCTTT TCCCCTCAGA AACGAACAAT CCAGAACCCA	180
CTGTTTAAAA CAACTGTATT TTGCCTTGGG AAGTCCCATT GCCTTCCCTG AAAACATTAA	240
ACATTCTCTC GATCCCCAGC CTGAGTCTCT CTGTCTCTGG GCCCATCCT GCTCCACAGC	300
AGGGCTGGTG TGTCCAGCAC AGAGTGACCC TCCGATGCC TTTCCACCC GCCGCCCTGC	360
CTCCCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GAATTCGGCC TTCATGGCCT AGGAAAGATC TAATTATCAT GGACCTGCCA CAGTTTCTTA	60
TGTGCCTGTC CCTGTGCACA GCCTTTGCCT TGAGCAAACC CACAGAAAAG AAGGACCGTG	120
TNCATCATGA GCCTCAGCTC AGTGACAAGG TTCACAATGA TGCTCAGACT TTTGATTATG	180
ACCATGATGC CTTCTTGGGT GCTGAAGAAG CAAAGACCTT TGATCAGCTG ACACCAGAAG	240
AGAGCAAGGA AAGGCTTGGG AAGATTGTAA GTAAAATAGA TGGCGACAAG GACGGGTTG	300
TCCTGTGGA TGAGTCAAA GACTGGATTA AATTTCACA AAAGCGCTGG ATTTACGAGG	360
ATGTAGAGCG ACAGTGGAAG GGGCATGACC TCAATGAGGA CGGCCTCGTT TCCTGGGAGG	420
AGTATAAAAA TGCCACCTAC GGCTACGTTT TAGATGATCC AGATCCTGAT GATGGATTTA	480
ACTATAAACA GATGATGGTT AGAGACGTTT TCGAG	515

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GAATTCGGCC TTCATGGCCT AGGGGACCTG ACGTTCAGTG TGGCCCAAAA GATGGCTGAG 60
 CCAGAGAAGG CCCCAGCCCT CAGCATCCTG CTGTACGTGC AGGCCTTCCA GGTGGGCATG 120
 CCACCCCTTG GGTGCTGCAG GGGCCCCCTG CGCCCAAGA CACTCCTGCT CACCAGCTCC 180
 GAGATCTTCC TCCTGGATGA GGACTGTGTG CACTACCCAC TGCCCGAGTT TGCCAAAGAG 240
 CCGCCGCAGA GAGACAGGTA CCGGCTGGAC GATGGCCGCC GCGTCCGGGA CCTGGACCGA 300
 GTGCTCATGG GCTACCAGAC CTACCCGCAG GCCCTCAGCC TCGTCTTGA TGACGTGCAA 360
 GGTATGACC TCAAGCTCGA G 381

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAATTCGGCC TTCATGGCCT AGCTCCACTT TCTCTGAAAA TTTATTCATA TTGTTAATTG 60
 AATTGTTTT TATTATAGAA ATAATATATT GCATGATTG TAAAAATGCA GAGGAACAGA 120
 ATGGCACAAA ATTATGTAAC CCTTCTATC TCCCTTGGT GTACCTCCTT AATCATACTT 180
 CTCAGAACCA TTGTCAATAA TTGCTGGGA GTTCTTCTGA TGGTTACCAT CGTGACTGAT 240
 AGATTTATTT CCCAGGTTCA AGCGGTTCCC CTGCCCTCAGC CTCCCGAGTA TCTGGGACTA 300
 CAGGCATGCA CCACCACTCA GCTCGAG 327

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTCGGCC TTCATGGCCT TGCCTTTTTT CTTTCACCAC TTTACTACAC ACAATTACTG 60
 GATTAATCTC TTTAATGCCG AGATCTTTTT TCCTTAGTGA CACCTTAATC ACTCTTAGCT 120
 TAACATATAT GGTATCCAT TACTGGGTTG CCTCTGCCTT TCCAGGATTG GCTGCCACTG 180
 CTCCTCCACA TACCCTGTAT TCTAGCCAAA TGGAACTACT GCTGTGTCCC AAGCAGATTC 240
 TTTATTTCTC TTGGCTGTTG CTCTCTATTT CTAATGCTAC CTGCCCTTCA AAACGAG 299

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATTCGGCC TTCATGGCCT ACTTGATTG TGGCTTATCT CAAGTTACCA TTTTTCAGTC 60
 AAGTCTGTTT GTTTGCTTCT TCAGAAATGT TTTTACAAT CTCAAGAAAA AATATGTCCC 120

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GAATTCGGCC TTCATGGCCT AGGGGACCTG ACGTTCACTG TGGCCCCAAA GATGGCTGAG      60
CCAGAGAAGG CCCCAGCCCT CAGCATCCTG CTGTACGTGC AGGCCTTCCA GGTGGGCATG      120
CCACCCCTG GGTGCTGCAG GGGCCCCCTG CGCCCCAAGA CACTCCTGCT CACCAGCTCC      180
GAGATCTTCC TCCTGGATGA GGACTGTGTU CACTACCCAC TGCCCGAGTT TGCCAAAGAG      240
CCGCCGCAGA GAGACAGGTA CCGGCTGGAC SATGGCCGCC GCGTCCGGGA CCTGGACCGA      300
GTGCTCATGG GCTACCAGAC CTACCCGCAG GCCCTCACCC TCGTCTTGA TGACGTGCAA      360
GGTCATGACC TCAAGCTCGA G

```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

```

GAATTCGGCC TTCATGGCCT AGCTCCACTT TCTCTGAAAA TTTATTCTATA TTGTTAATTA      60
AATTTGTTT TATTATAGAA ATAATATATT GCATGATTG TAAAAATGCA GAGGAACAGA      120
ATGGCACAAA ATTATGTAAC CCTTCTATC TCCCCTTGGT GTACCTCCTT AATCATACTT      180
CTCAGAACCA TTGTCAATAA TTGCTGGGA GTTCTTCTGA TGGTTACCAT CGTCACTGAT      240
AGATTTATTT CCCAGGTTC AGCGGTCCC CTGCCCTCAGC CTCCCGAGTA TCTGGGACTA      300
CAGGCATGCA CCACCACTCA GCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

```

GAATTCGGCC TTCATGGCCT TGCCTTTTTT CTTTCACCAC TTTACTACAC ACAATTACTG      60
GATTAATCTC TTTAATGCCG AGATCTTTTT TCCTTAGTGA CACCTTAATC ACTCTTAGCT      120
TAACATATAT GGTCAATCCAT TACTGGGTG CCTCTGCCTT TCCAGGATTG GCTGCCACTG      180
CTCCTCCACA TACCCTGTAT TCTAGCCAAA TGAATCACT GCTGTGTCCC AAGCAGATTG      240
TTTATTTCTC TTGGCTGTG CTCTCTATT CTAATGCTAC CTGCCCTTCA AACTCGAG      299

```

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

```

GAATTCGGCC TTCATGGCCT ACTTGATTG TGGCTTATCT CAAGTTACCA TTTTTCAGTC      60
AAGTCTGTTT GTTGTCTTCT TCAGAAATGT TTTTACAAT CTAAGAAAA AATATGTCCC      120

```

```

AGAAATTGAG TTTACTGTG CTGTATTTG GACTCATTTG GGGATTGATG TTACTGCACT 180
ATACTTTTCA ACAACCAAGA CATCAAAGCA GTGTCAAGTT ACGTGAGCAA ATACTAGACT 245
TAAGCAAAAG ATATGTTAAA GCTCTAGCAG AGGAAAATAA GAACACAGTG GATGTCGAGA 300
ACGGTGCTTC TATGGCAGGA TATGCGGATC TGAAAAGAAC AATTGCTGTC CTTCTGGATG 360
ACATTTTGCA ACGATTGGTG AACCTGGAGA ACAAAGTTGA CTATATTGTT GTGAATGGCT 420
CAGCAGCCAA CACCACCAAT GGTACTAGTG GGAATTGGT GCCAGTAACC ACAAATAAAA 480
GAAGTAGTCT CGAG

```

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

```

GAATTCGGCC CTTTCATGGCC TACTCCCGAG CTCTACTGAC TCCCAAAAGA GCGCCCAAGA 60
AGAAAATGGC CATAAGTGGG GTCCCTGTGC TAGGATTTTT CATCATAGCT GTGCTGATGA 120
GCGCTCAGGA ATCATGGGCT ATCAAAGAAG AACATGTGAT CATCCAGGCC GAGTCTATC 180
TGAATCCTGA CCAATCAGGC GAGTTTATGT TTGACTTTGA TGGTGATGAG ATTTTCCATG 240
TGGATATGGC AAAGAAGGAG ACGTCTGGC GGCTTGAAGA ATTTGGACGA TTTGCCAGCT 300
TTGAGGCTCA AGGTGCATTG GCCAACATAG CTGTGGACAA AGCCAACCTG GAAATCATGA 360
CAAAGCGCTC CAACTATACT CCGATCACCA ATGTACCTCC AGAGGTAACGT GTGCTCACGA 420
ACAGCCCTGT GGAAGTGA GAGCCCAACG TCCTCATCTG TTTCATCGAC AAGTTCACCC 480
CACCCTCGA G

```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

```

GAATTCGGCC TTCATGGCCT ACCTTATCTT CTTAACCTTT CAAATACTTG CAGATATTTT 60
GCTTGGTGCT TCCCATCTAT TGCAATACCC CTTTAGATAA AGTCAATTCT TATCTAAAAT 120
CAAATTCATT TTATTGACA ATGTTTACAA ACAACCCAG GACGATAACA ATTACACTCT 180
CAATACTGGC ATCACACCTT CACAATTACA CTAACCCCAA CCTAGGCCAT GAAGGCCTCG 240
AG

```

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GAATTCGGCC	TTCATGGCCT	AGACAGAATT	ACTGGGAACC	ATTTTCCAAG	TAGCCCACCA	60
CAAAGGTTGT	ATTTTGTCAA	ATTGAAGGAG	TCATCTGACT	TTCTTAATC	ATAAGCTACA	120
AATATAATAA	GCTACATTAA	TAGATTTTCT	AATATTTATT	TAACTTTGAA	TTTCTGGAAA	180
AAACCCAAC	TGGTAATGAT	TTATCATCTG	AGCTTTGTTT	TTGGCTTTGG	TATGCTAATT	240
TTTGCTTAG	GATTTTATA	TCTATTTTAT	GACTGGCACC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GCACGCCATG	GGAGAAAAG	AAGAAGCCAA	AAAAACAGAA	GACAAGTCTT	TGCAAAGCC	60
TGAACTGAT	AAAGAACAGG	ACAGTGAAAT	GGAGAAGGCT	GGAAGAGAAG	ATATGGATAT	120
AAGTAAATCT	GCAGAGGAGC	CACAGGAAAA	AGTTGACTTG	ACTCTAGATT	GGTTAACTGA	180
AACCTCTGAA	GAGGCAAAAG	GAGGAGCAGC	ACCAGAAGGA	CCGAATGAAG	CTGAGGTCAC	240
TTCTGGGAAG	CCAGAACAGG	AAGTACCAGA	TGCTGAGGAA	GAAAAATCAG	TTTCTGGAAC	300
TGATGTCCAA	GATCTCGAG					319

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GAATTCGGCC	TTCATGGCCT	AGACACATAC	AAAGATAAGG	CTTTGATAAA	ATTCAAGAGT	60
TATTTGTATT	TTGAGGAAAA	AGACTTTGTG	GATAAAGCAG	AGAAGAGCCT	GAAGCAGACT	120
CCCCATAGTG	AGATAATATT	TTATAAAAT	GGTGCAATC	AAGGTGTGCG	TTACAAAGAC	180
ATTTCTCGAG						190

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GGATTGAATT	CTAGACCTGC	CTCGAGTAAG	ACCCCTTTTT	AAAATGACTC	CCACTGTCTA	60
TTCCACAGCC	GGTGTGCGGC	ATGCTGATT	AATCCCCACA	ACAGCCCAGG	AGGTAGGCGC	120
CGTCCCATCC	TCCTTTACAG	GAGGGGAAAC	TGAGGTTT	GTGGTCAGAT	GGTCAGCTGC	180
CTCCAAGACC	ACGCTCGAG					199

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

```

GAATTCGGCC TTCATGGCCT ACCTGTACCT GTTTTATACT TGCTTTTGCT TCAGCGTTCT      60
GTGGTTGTCA ACAGATGCCA GTGAGAGCAG GTGCCAGCAG GGAAGACAC AATTGGAGT      120
TGGCCTGAGA TCTGGGGGAG AAAATCACCT CTGGCTTCTT GAAGGAACCC CCTCTCTCCA      180
GTCATGTTGG GCTGCCTGCT GCCAGGACTC TGCCTGCCAT GTCTTTTGTT GGCTAGAAGG      240
GATGTGCATT CAGGCAGACT GCAGCAGGCC CCAGAGCTGC CGGGCTTTTA GAACACTCCT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

```

GAATTCGCCC TTCATGGCCT ACCCAATTCA GTTCCAGAG GAGGTGGAAC CTCTGCAAC      60
CCAAACAGGAG GCCCAATTG AGCCTCCAGT TTCTCCTATG GAGCATGAAC TTCCATCAG      120
TGAGCAGCAG CAGCCAGTTC AGCCTTCTGA GTCTTCTAGG GAGGTGGAAT CTCTCTGAC      180
CCAGCAGGAG ACCCCAGGTC AGCCTCCAGA ACATCATGAA GTCACAGTTT CACCTCCAGG      240
TCACCATCAA ACTCATCATT TAGATTCAAC CAGTGTCTCT GTGAAGCCTC CAGACGTGCA      300
GCTCACCATA GCAGCAGAGC CTAGTGAGA GGTGGGAAC TCTCTAGTCC GACCCCTCGA      360
G                                     361

```

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

```

GAATTCGGCC TTCATGGCCT ACCGAGATGG AAATAACCTA AGAAAAAGAG GGCATCCAGC      60
TCCATCTCCC ATTTGGCGTC ATGCTGCTCT GGGTCTGGTA ACTCTTTGCC TGATGTTGCT      120
GATTGGGCTG GTGACGTTGG GGATGATGTT TTTGCAGATA TCTAATGACA TTAATCAGA      180
TTCAGAGAAA TTGAGTCAAC TTCAGAAAAC CATCCAACAG CAGCAGGATA ACTTATCCCA      240
GCAACTGGGC AACTCCAACA ACTTGTCAT GGAGGAGGAA TTTCTCAAGT CACAGATCTC      300
CAGTCTTAAC CTCGAG                                     316

```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

```

GAATTCGGCC TTCATGGCCT AGGCAATATC AAGSTTTTAA ATCTCGGAGA AATGGCTTTC      60
GTTTGCTTGG CTATCGGATG CTTATATACC TTTCTGATAA GCACAACATT TGGCTGTACT      120
TCATCTTCAG ACACCGAGAT AAAAGTTAAC CCTCCTCAGG ATTTTGAGAT AGTGGATCCC      180
GGATACTTAG GTTATCTCTA TTTGCAATGG CAACCCCCAC TGTCTCTGGA TCATTTTAAG      240
GAATGCACAG TGAATATGA ACTAAAATAC CGAAACATTG GTAGTGAAAC ATGGAAGACC      300
ATCATTACTA AGAATCTACA TTACAAAGAT GGGTTTGATC TTAACAAGGG CATTGAAGCG      360
AAGATACACA CGCTTTTACC ATGGCAATGC ACAAATGGAT CAGAAGTTCA AAGTTCCTGG      420
GCAGAAACTA CTTATTGGAT ATCACCACAT CTCGAG                                456

```

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

```

GAATTCGGCC TTCATGGCCT AGATCATTCA GTGGCTCACC TAATATCACA GAACAAGTGG      60
TGGAGTCAGA ATCTTTTATC TAAAGGAGAT ATTTTCATCC TTAGATTAAT GTCCTCTTCA      120
CAGTCTCATG CTACTTTCCT TTAAATGAA ATTGCTGTTT TTTTITTAAT TGATTGGGCC      180
AATTCATTT GTAACGGAAG AATCAAAATT AGAGCCCGGG TCTCATCCTA CGGTATCTCG      240
TCCTGAACCT CTGGTCTCCC TCAAGAATGA CTCAGAAGGA CGGACTCGAG                                290

```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```

GAATTCGGCC TTCATGGCCT AAAAAAAAAA GCCTTTTAAA CTGTAGGAA TTAAGAAATA      60
AGAATAACCT ACAAATGCT AGCAAAATT ATCTCATTTT TTTTCATTGT ATTTTCAGGT      120
TTAACTGAAC TGAATGACAG TCCAGTTCCT CTAGAACTTG AGCGCTGCAA GTCTCCTACC      180
TCAGACCATG TAAATGGACA CTGCACAAGT CCAACTTCTC AGAGTTGCAG TTCTGGAAAA      240
CGTCTTTCTA GTGCCGATGT TTCAAAAGTA AATCGCTGGG GTCTGGAAG ACCACCAGTT      300
CTCGAG                                306

```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

```

GAATTCGGCC TTCATGGCCT AATATTTATT AAATGACTTG GTAGATAGAG CAACTGACTG      60
AATATATTAT TTTTATAGAA GAAGAAGAAC ATTTTGGCTT AAATTAAATT TCTTATTTTA      120
TTTCTCTTTC CCCTTTTATC CAGGGTAGGT CCAGGTAAAG CCAAAGGCCT TATCCTTATC      180
TACACTGCTG GGGGACACAA CACAAGAATT TCAAGTTCAA GTATTATTTC TCATTTTGAG      240
TAATTTTGTT CTCATTTTGT TCCAGTTCTC ACTCTCAGAA AAAGATTACT CGAG      294

```

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

```

GAAACAATAG AAACACTGAG AGAAAATTCA GAGAGACAGA TTAAGATACT GGAACAGGAA      60
AATGAACATC TGAATCAAAC AGTGTCTTCC TTAAGGCAGC GGTCCCAGAT AAGTGCAGAA      120
GCAAGAGTGA AAGACATTGA AAAAGAAAAC AAAATTCTTC ATGAATCTAT CAAAGAAACA      180
AGTAGCAAGC TAAGCAAGAT TGAATTTGAA AAAAGACAAA TTAAGAAAAGA ATTGGAACAT      240
TATAAAGAAA AAGGAAGCTC GAG      263

```

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```

GAATTCGGCC TTCATGGCCT ACCTGCCCTT CTGCGGTCAC AGCTGCCTGC TGGGTGGGAG      60
TCCGGGGGAA TGGTATGTGT GGTCACCAGA GGGCACTGAG TGGGCTTCAG TGGCATGTGA      120
ATCCTGGCAG AGTCTCGGAT CCCCAGATGG GAGAGGAGAA AGCACAGCC AAGACAACGA      180
GTGGGGGAAG GAGGCAGGGG CTAAGTGACG GGTGGGGGGT GGGGGTGGGA ACTCCAGTGT      240
ACACATTGAC AGTCTCTATG TTGGCTTCAC CAGCGCTTCT CTGTTTGTCT CGTCCCTGGA      300
TTTCTAACAG TTGCCTCGAG      320

```

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

```

GAATTCGGCC TTCATGGCCT AGTCGGGAGT GTCTTAAGCT TTTCATTAA CCTAAAGTAC      60
AGAGTCTGCT CTGTAGAAAT ATGTCATTAA GAAAATATTT GAGTCCCAGC TCCTCCTTGT      120
TGTGTAATGT CTGATAATT CACTCATTAA ATTACCCAGA CAGACCATAA AGTCCTCTCA      180
GTTTGCATCA CCTGAAAGTC AGTCAGCCTG GGCTGTGAGG ATTGTGAGGT AGAACTCACT      240
GTGGAAGGAC GGCATTAGGG AAGACTTTAG GAAAATGGAG CGGAACCTCG AG              292

```

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

```

CTCGAGACCT GTGTGCGCAG GCAACGGGGA AACTGGAAAT GCGTTGACAA ACTGACGCAA      60
AACTGGGCCC AACAGCCACA AGGCACGGT CGTTTCCAC TGGGCAAAGT TCAGTCGCAT      120
TTCTTTCTGT TCTCTTTCTT TCTTTCTTTT CTTTTTCTC TTTCTTTCTT TCTTTCTTTC      180
TTTCTTTTTT CTTTCTCTCT CTCTTCTGT CTGTCTCTCT CTTTCTTTCC TTCTTTCCTT      240
CCTTCCTTCT TTCTTTCCTT CCTTTCCTTT CTTTCTTTT TTTTCTTTT AAGAGACGGA      300
GTCTCGCTCT GTTACCCAGG CCGGAGTGCA ATGGCACAAT CTCGGCTCAC TAGGCCATGA      360
AGGCCGAATT C                      371

```

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

```

GAATTCGGCC TTCATGGCCT AGTTCCTTGG TGGTTTGAAA GTTAGAGAGA TCCTGATAAG      60
CATAATGACC AACATAGAAG AGATTAAGTA CCTTTACTCA TAAATGTGAG TTCACAGACT      120
TCAGGTCTAA ATTCGTAACA ATATTTAAGA TGTATATGGC TTAAAGTGCT GGTAGTTTGG      180
ATTAGAATCC ATAGGTTTCT AGTCACTGCT CTTTTCATTA TTTGAGTTT TATGTATTTT      240
TTAACTAGAA ATAAGAGGGT CTCGAG                                           266

```

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

```

GAATTCGCCT TCATGGCCTA GAAAGTTTTT CAAAAATTCT TCAATTGTCT CTGTTGATG      60
CAACTTAATT TTTTGCTGAG AGAGACCTTA AATGTAATTA GTATTGTATA ATTASCTGA      120
TTAATCTGAC CTGTACATCA CGAGTCACTT GTCTTTAGCC CAAGAGGAAT GCTTCCTTTC      180
TGATTGAGG CAGTGGCCCA TCATTGCTTC TAGCAACCTT CCTACTTACT AGATGACCTT      240
GAGTCAAGGT TTCTGTATAT ATGATTTCAG ATTGTGCCCC TAGAACTGAA AAAGGGTAGG      300
AGAGGCAAAG ATAGGAAAAA TATTTTTTAA AAATTTTAA GTATTTTATT TTTATTGGGA      360
AAATATTTAT TGTAAGTCTT CCATTTGTTA TCCTTCTGCC ACTAGCATTG CGTAAAAAGT      420
AAAAAGAGCT TTACATCAAA AAGCACAATG AAACCTTTGTA TCCTTAAGTC CGTACTCGAG      480

```

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

```

GAATTCGGCC TTCATGGCCT AGTCGGAGGT GTAGGAGGGG CCGTGGAGGT CCAGGTGACT      60
GCTTAGAAAA CTGCACAGCA TCTGATGAAA TTAGCGAATA AGAACATCAA CCATGTCTTA      120
CACTCCAGGA GTTGGTGGTG ACCCGCCCA GTTGCCCGAG AGGATCTCTT CTAACATCCA      180
GAAGATCACA CAGTGTCTTG TGGAAATACA AAGAACTCTG AATCAACTTG GAACACCTCA      240
AGATTACCTT GAATTGAGCC AACAGTTGCA ACAGAAGCAG CAGTATACTA ACCAGCTTGC      300
CAAAGAAACA GATAAGTACA TTAAAGAGTT TGGATCTCTG CCCACCACCC CCAGTGAACA      360
GCGTCAAAGG AAAATACAGA AGGATCGCTT AGTGGCAGAG TTCACAACAT CACTGACAAA      420
CTTCCGAAG GACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```

GAATTCGGCC TTCATGGCCT AGCTACCTAT CTACAAAAAC TCCTGGATCC TTTATTACGA      60
ATTGTGATCA CATCCTCTGA TTGGCAACAT GTTAGCTTTG AAGTGGATCC TACCAGGTTT      120
GTCATCTTTT CACATAGAAC CGCTGTTTTT TGTTTTTTTT TTTTGTTTGT TGTTTTACT      180
AACTGTCAT GAAGCAAGGC ACCTTCTCCC CTGATCATT AAAATTAGTT TTAATTATA      240
AAAGTTATAT ACAAATACAC GTTCTTTTAA TGATATCTGT AATTTTTTTT TAAGGTATCC      300
TTTTATTTGC CTTAGATCCA GGGACAAACT AGAGAAAGGT GTCTTTGACT TCCACCTCCA      360
GAGACTGTTA CTAGTTAAGT CTGTTCCCCT GTCCTTTTTC CATGCACCGC CTCGAG      416

```

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

```

GAATTCGGCC TTCATGGCCT AAGGAGGTCC ATGAGGAAGT GTCCCAGCCT GTCAGTGCAT      60
CTCATGAGTT CGCTAGTGA TCAGCAGACA GTTCCAGGAA GTGAACAAGT CCAAGAGGAC      120
TTCTGATTAG TCCACAGTCT CCTCTATAGG CTCAGTAGAT GAAGGCGTTT CTGAGGGCTT      180
GCCTACACTT CAAAGCACGT CTAGCACTAA TGCTCCTCCG GATGATGATG ATCGATTGGA      240
AAATGTTTCTAG TATCCCTACC AACTCTACAT TGCTCCTTCC ACCAGCAGTA CAGAGCGACC      300
AAGTCCAAAT GGTCCCAGCA GACCTTTTCA GTGTCCAACC TCGGGGGTGC GATTACCCCG      360
TATTCAGAAC CTAAAGCAGC ACATGCTCAT CCACTCAGGA ATTAAACCAT TTCAGTGTGA      420
CCGCTGTGGG TCTCGAG                                         437

```

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

```

GAATTCGGCC TTCATGGCCT AGATCACTGC CCTTTCAATA ACACTCTTGC CTCTAGAATC      60
ATATGTTCAA AGTATGAATA CACACCTAGC ACATAGTAGG TGCTCAAATA TTAATTTTCT      120
CCTTGCTTTC CTTATCTACC CTGTGTCTTC CATTCCCCG TATGATTCCA ACCCAATATA      180
GCAAATGACA TTTACATGTT ATGAAAACAT CTATTGGGTA AAATCAGATC TTGGATAAAG      240
AAATTCTGAC TTTTATATAA GCTTTTGGTA GACAGAAAAA ACAGAAAGGT ATTTCGTTGGT      300
AGAACATTTT TAAGTTCAGG AAAGAAAGCT GGAATAATAC TACGTAACCT TGTCAGGTT      360
ACTTTGACTG AAACACGTTT TTGGTGGATT TCTTTTCTTC AAAGAACTCT CTAAATGCAA      420
CTCCTTGCTG GATTCTCAC CCGATCTCGA G                                         451

```

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

```

GAATTCAACC ATTAAAGATA ATTTATATTA GTGTTTCTAT AACTTCTAAA ACATCTTTTG      60
ATAAGGATAA TAATCTCATT GTCATTCTGT ACTGATATTT GGATATAATC CTAGCAGGGC      120
ATAGCTCTGA TTAAGAACAA TTGAACCAT CAAATTTTITA TTAGCCTCTA TTTTCACTAG      180
CCAGGATATT TTCATGAAC TTTTATGTTT CAAAGCAAGT TTTTCTTTC CAATAGAAAG      240
TGTATATTA GTAAACAATT TTGTCTTCTG CCAAGACCAG CTCAGTCGGG AAGATCCTAA      300
CCCAAGTGCA AACTCGAG                                         319

```

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

```

GAATTCGGCC TTCATGGCCT AGGGAAGAAT AAAGAACAAA ACCCAAACT TTGGACCTTA      60
AAAAACCCAG GCTGGCATT TAGTAGCAAT TGGGTGTGTT CGGTTTGTAA TATATTGTGA      120
TATACATGCC TCCATGTGCT TTGSCCTTCT GGTATCTTCA CCAGATGCTG CCTTTTTTTT      180
TTTTTTTAAAC AAGTTCCTGT TTCACCTTTC CAGCTAGCTG CTGGGTATCT CCAACAAAAT      240
ATCTCATAGA TCTCCCACT GTAATGTATT CAAGCCAAA ATCAGCTCTG CCCATTCTCC      300
ATCCCAAAGC CCCTCCTCTT GGTACCAGA CAACCTTAAC CAAACCACTC GAG              353

```

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

```

GAATTCGGCC TTCATGGCCT AGAGGAGGAA GGCCTTCGTA AAGGTTGCAT CTCCGTCCCT      60
TCGCTCCCGG GGACCCGCGG GAAAAAATAA AATCCAACAC CCAGGCCCCG CGGCTAGCCC      120
CTTCCACAG GCTCTCTCCG CTCGATTTTG TCACCGTTAT GTGGGAAGCG AATCCATGTA      180
TTTGCAAGCC CGAGTCTTTG AGCCGTGCTA TACCAGTTTG TCCAGATTGT TTATACTAGC      240
AATGCAGTTT ACGGTGAAGA CCTGCCTTCC CTCTGGGAAT CTGGAGCTTC AGTAACAGGA      300
GATGTTTCAC AAAGCAGAAG AATTATTTTC TAAACAACA AACATGAAG TGGATGACAT      360
GGACACGTCA GATACCCAGC TCGAG              385

```

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

```

GAATTCGGCC TTCATGGCCT ACTCCGTCTC CAAAAAATAA AAAAAATAGT GTTCAGCAAG      60
GTTGAAGCAT AAAAGGTAA TAGCCAGAAT CATTATCAA TTGTATTTCT ATACATCTAC      120
AAGACACAAT CTGAAAATGA AATTAGAGAA ACAATTTTAC TGGGCAACAA GAGCAAACT      180
TCATCTCAA ATAATAATA TAATAATAAT AATCATCATC ATCATCATCA TCTACAATGT      240
CATTTCCCAT CCAAGTCTCG AG              262

```

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

```

GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAGCTCCTG GCCTCGGGCA CTCTACCCGC      60
TTCAGCCTCC CAAAGTGCTG CGACTGATTA CAAGTATGAG CCACTACGCC TGACCATAAC      120
ATGTAAATTT ATGGCAAATG GTAATTCACA GCTCAATTCT AAAATGTGAT GAAATTTAAA      180
TCAGAAAGGC CAAATGAGTC ACTTTTCTT AACACTAAGA ATTATAAACC TTAAATTTTC      240
TTTGTAAGTG TAATTTTATA TGTGACATGT ATATGCTTTT TAATATGTGT GATAGGATGA      300
GGGGCAGGAG AGGGGGCTCT AGACATGAGG GTGCCTGGGG CCTCTGTAGA CCTTCAGATG      360
GCCCTGGGTG TTATAGCAAG AGCTGGTCTA CATCTAATAC TACTGCAGG? GCTGTCATGA      420
ATTCTTTGTA TAATTCCTTG TATATTAAAT GACATTATTC TATGTATAAT GTCATTTAAT      480
ACTTATAACC TACTTTCCTC GAG                                         503

```

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

```

GAATTCGGCC TTCATGGCCT AATGGATTCA TTTTTTTTCA GCAGCATGGC ATAGTGGATT      60
ATGAAATCAA AATTAACTAC ATGTGGAGTC NTACATTGAA ATCCCCCTTC AACAAAATAG      120
TATACTATGA GTATTTTAA ATTATTTAAC CCTCCGAAC ACCAATTTGT ACACGAATAA      180
AACTTGACAC AACAGGATTT TGTGGGGCGT GAGTAACACA ACATATACAA AAGCACCTTA      240
TAAAGTGTTT TATATAGCAA CTCTCTCTC AGTTTGAACG GGTCTCAGGA TAAATTAGCA      300
AATATGAATT CTAACCTTTG TACTTACATT TTAATTCTGC TAAGTGTGTG AACCCCAATT      360
TAGCAATTAA AATATTTATT TCCAGAATGT TTTGACCCTG AGCATATTTT TAAAAAGCAC      420
AGTAGCTCGA G                                         431

```

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

```

AAAAGTGACT GAAAGTTTGC TAGTGTTTT AGTACCGATA TTTACTGGTA GTAAATATAT      60
ACTAAATCCA GTGAAATATG ACTTCTCTAA CTGAGCTTGA CATATCCTGG TTATATCTCA      120
TGGCAGCTGA AACTAGAAA TGACTTATTT TTACCTTGTA GCCACAGCAC ACTTGAGGTT      180
ATTCTTAGGT TTTTGTAGA GACAAAGCTG GTTAGTGACT CCTGGATTAA GAATTATGAG      240
TGATCCATA ACCCTCGAG                                         259

```

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

```

GAATTCGGCC TTCATGGCCT AAAGGATATT GGCATGTTCC TCTTCTCATC AATATCCTAA    60
AAGACATTTA TTTTTCACAC ACTCCTTGGG AAAAATTAAC TTTTTCAC TGAAAATATT    120
TCCTTTTGTG GTTATCTTGA TCTCAGATTA TTTTGTGAAA GAATTTTACT GTACTTAGTT    180
CAAAAGAGTA GAAAGAATGA TTTACTATTG CAGACATATG TAGGGTAAAA TCATAATTTA    240
TTTAACTGA CTGTACAACA CCATTTAGAG TTGATATTGA CATAAATGTT ATTAGCCTAC    300
TAATTTGGAA CTGCATTCT CAACAATGCT GGCAAGCATC TTCCGTACTT AGCATACCAA    360
GTTGTAGGGG AGAGACTGTG TATATATTTT TTTAAAGCAA TCCAATGGAT TTGTTTTGT    420
TCATATTTTG GAAACAAC TCAG    443

```

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

```

GAATTCGGCT TCATGGCCTA CAAAAGATGG CCCTAAGCCT GGCCTCTAGC TTTCACTCGT    60
GGTGAATATT TCAGACCTAA AGATCCAGAT AGTATCTCTG TTCATATGTG AATAAGTTGA    120
AGATTGTGGG GCTACTTTT CTCATAGCAC TTTATTTTGA ATGTTGTTAG TTTGTGCTGA    180
GAATGGTCGT CCGTATTGA ACCAATTATT TATTTTAAAA TATATTTAAG CTACATTTT    240
GTTTTGAAAA ATTGCCATAA ATTTGGTGCC ACTTTCTTTT ATTTATTTGA CTGAGTTAAT    300
ATTATTGTAT TAACATTTA AGTATATGGT GTTTACATTC TTATTCTTT TGACATTTTG    360
GAAATAATCA TAACTGTCT TCCAAAATA ACCATTTCT TGATGGAAC CTTCCTAGAG    420
TTTTTACCAA ATAGCTAACT TTAGTAGTAA AACCTCATTG TGTATCCATT CCCCCACTCG    480
AG

```

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

```

GAATTCGGCC TTCATGGCCT AGATTGTCTAG TTTATCTTAG ATGATGAGGA AGCAGTACCA    60
AGAAAACACT TGGGGGTTGA TACAACAGGC ACATGAGCCC TTAAACTCC TTCCTGTTTT    120
TTTCTTTTT TTTTCTCTT AGGTAGATTA GTGCATTAA AGCCTGAAGT TAATTGACC    180
TAAATTTTT ATAAGTCTT GCAGAAAGT CACTTGTTT CTGAAATCAT CTCCTTGATA    240
ATTTTTTATG TAACAGTTGT TCATATTGTA GGAATGATAT ATATGTCATC CTGTTACACG    300
TGTCAAGCAC TTCAAAAAGA CTCCAAGAGA ACATGCCTGA GAAAGATAAC TCCCAATTAA    360
AAATGATTCA GTCCCTCACT TGCAATATTC AGGATAAATG TGTGGAAACA TTAGGCTACC    420
AGATAAATAA AAGGTAGTTA TTTCTAGGG TGA CTGCA AGATATTTCT CGAG    474

```

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GAATTCGGCC TTCATGGCCT AGCCTTTGAG ATCAATACCT GTGAAAAGTA GGGAAAGAAA	60
GCAGATGAGG CATAGGGAAA AGGTGGACTG CCACAGGCAA CCCAGCGAAC CTCACCAGCA	120
GCTCTGGAGC TAAATAGCT CTTCAGAATT GTCCAGAGTT GGGCTGAGGA GGCCAGAATT	180
TTATTTGTGT TCCCACGATG ACGACTTCGA G	211

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

GAATTCGGCC TTCATGGCCT AAATACCTTA ATGGTGGTAG AGCCTTTACC TGTAGCTTGA	60
AAGGGGAAAG ATTGGAGGTA AGAGAGAAAA TGAAAGAACA CCTCTGGGTC CTTCTGTCCA	120
GTTTTTCAGCA CTAGTCTTAC TCAGCTATCC ATTATAGTTT TGCCCTTAAG AAGTCATGAT	180
TAACTTATGA AAAAATTATT TGGGGACAGG AGTGTGATAC CTTCCCTGGT TTTTTTTTGC	240
AGCCCTCAAA TCCTATCTTC CTGCCCCACA ATGTGAGCAG CTACCCCTGA TACTCCTTTT	300
CTTTAATGAT TTAACATATCA ACTTGATAAA TAACTTATAG GTGATAGTGA TAATTCCTGA	360
TTCCAAGAAT GTCGAG	377

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

GAATTCGGCC TTCATGGCCT AAGGCGTTTG GGGTTTCCTA GTTGTGCTGC TGCTCTTGCC	60
TAGGGAATCT GCTCTTGCTT TGGCCTCTTT CCTTGGGGCA AGAGTGAGGG GGACAGGGAG	120
CTTCAAGTCA GCCCTCCATG TTGAAGTTTG GTAGAAGCTC TGCCACACCC TTGGACTGGA	180
ACCCAGCCAT GCCAATCCCC ATGATCACCA ATCCGAACCC CTTGAAGTAG AATTTTCATA	240
CCCTACTGAC TAACCACCTT CTTAGCCAGG CCATAGCCAT TCAGCAGTGC CTCCTTCCTC	300
TGGGTAGACA AACAGCCTTG AACAGAAAGG TGGAACACTC GAG	343

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

```

GAATTCGGCC TTCCTGGCCTA GAGTCCTTGT TGTCTTTTGC AAAGGTTGCT CATCACCTCT      60
CCCCTCCCTC TGGCTCTTTT CCGTGGTGAT GCATAGTTCA ATGCGCCACG GAAGCTTCAT      120
GATGAGGCCG TCACCCAAAC TAGCAGCCCT CCTTTCCTTC TTTCTTTGCC AAGTGTCTCG      180
GACATCAGCT CTTCTCAGT CTTTGACTCT AAATAAGAA CTTGAATTTC ACCATTCAAC      240
TGAAATCCCT CTAACCTCG

```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```

GAATTCGGCC TTCATGGCCT ACACCGTCGC CATTGCCAGA AAGAGCGATT TATGGCTTTG      60
TTCTTTTCTT AAGCTCCCAA TTTGGCTTCA TACTTTACCT CGTGTGGGCC TTTATTCCTG      120
AATCTTGGCT AAATCTTTTA GGTTTAACCT ATTGGCCTCA AAAATATTGG GCAGTTGCAT      180
TACCTGTCTA CCTCCTTATT GCTATAGTAA TTGGCTACGT GCTCTTGTTC GGGATTAACA      240
TGATGAGTAC CTCTCCACTC GACTCCATCC ATACAATCAC AGATAACTAT GCAAAAAATC      300
AACAGCAGAA GAAATACCAA GAGGAGGCCA TTCCAGCCTT AAGAGATATT TCTATTAGTG      360
AAGTAAACCA AATGTTCTTT CTTGCAGCCA AAGAACTTTA CACCAAAAAC TGAAGTGTGT      420
GTAACCATAG TAACACCAAG CACACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

```

GAATTCGGCC TTCATGGCCT AAATCTTCAG GGTCTTAACT TAGTTTTTGA TCCCTAAAAT      60
TAGTGCTGCA TATGTAGACT CAGAAACCTC ACGTAAAAAT TTAAATTGGC CTCAGGTTGG      120
CAATGTTCCA AGGCAATGGT TAGAAGCAAA TTCAGATTCT CCAAGGCCTC AAATAATTCC      180
TACAGATAAA ATCCCAAGGA AATTCAGCAG TGCCTAGTCA AAAATCCACA AATCAGGCTC      240
GAG

```

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

AAGCGAGGCC	CTGGGGGACA	ACGTGAAACA	ATACTGGGCT	AACCTAAAGC	TGTGGTTCAA	60
GCAGAAGATC	AGCAAAGAGG	AGTTTGACCT	TGAAGTCAT	AGACTTCTCA	CACAGGATAA	120
TGTCCATTCT	CACAATGATT	TCCTCCTGGC	CATTCTCACG	CGTTGTCAGA	TTTTGGTTTC	180
TACACCAGAT	GGTGCTGGAT	CTTGCCTTG	GCCAGGGGGT	TCCGCAGCTT	CTCGAG	236

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

GAATTCTAGA	CCTGCCTCGA	GCCTGCAGAC	ATCTCCTCCT	TCTTTGTGGT	TCTGGGAGCC	60
ATTCTGTGCC	TCTAAGGTCC	TCCTTCTTTT	TTCTCACCAA	TACACATATT	TTCTGTCCTT	120
CGCAATTCTA	TTAAACCTCA	CATTTGATGG	TGTTTTCTT	AAAATTCCTT	TACTTGGTTC	180
CTGCATTCTT	CATTCCTTCC	CAGCACAAATC	TCGAG			215

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

GAATTCGGCC	TTTCATGGCCT	AGAAGAAAAC	CCATCAGATA	TTATAATAAG	ACAATAAATC	60
AATTCAGAC	TTGTAAACAA	AGGTGACATT	AATCTATTGA	AATGTGGGAA	AATAGTCAAC	120
CTGTATCCTT	CTCATACCAT	AAATCAGCAT	GTTTGATCAC	TGGAAGCTTC	ATTTTGATGA	180
TTAGCAGTCA	TGTATTGAGG	CTAAATGATA	TGTTTGTCGC	ACAGCATCTC	GAG	233

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

GAATTCGCCT	TCATGGCCTA	CACAGGAGAA	AAACCCTATG	AATGTAGTGA	ATGTGGGAAA	60
ACTTTTGTTC	AGAAGTCCAC	CCTCAGAGAT	CATCACAGAA	TTACACAGG	GGAGAAATCC	120
TTTCAATGCA	ATCAATGTGG	AAAAACATT	GGCCAGAAGT	CAAACCTCAG	AATACATCAG	180

AGAACTCACA CTGGGGAGAA AACTTACCAG TGTAATGAAT GTGAAAAATC CTTCTGGCGA 240
 AAAGATCATC TCATTCAACA TCAACTCGAG 270

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

GAATTCTAGT TTAATTACAT ATACCTCTCT GTTGGCTTAG TAGTAATAAA AATATTTTCT 60
 GTAGGTGTAG AATATCCTTA CAGTCCAAAA GGAGAGTACA TGTCACAAT TAAAGTTTGA 120
 AATTTGTGCT TTGATAACAG CATGTTTTAT TCATTCATTT TTATAATAAT ATTACTGAGC 180
 CTGTATCATA TAGTGATGAA CTTTTCAGCT GTTTTGAGGG TTTGTGTTAG CCACATTCAC 240
 ATTTGTATAA CCTGTGTTTC TTTTITATTT TTCTTTATTT TCATTTTAGA TTCAGGGGGT 300
 CGGCTCGAG 309

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

GAATTCGGCC TTCATGGCCT AAGCTCTTTT AGTGAAGGAT TGTTTTAAAT AAGAGCTCTC 60
 AGTTCAAGAC AACTACTGTT AGGAGCTTAA ATCGGAACCA CAATCAGCAT ATAAAGGTCC 120
 TAATCCTGAC CTTAATCCCT TTGGAATATT GGTTTTATAA ATCATCAATC AACAGTGTTC 180
 CACTATGAAA GCATATTCGT TCTTCTTCTT TTCATGTATT CCTTCACTGC TGGTGCTTAA 240
 TGTCTTTCCT TCCTCTTCTG CCATTTCTCT TTCCATGAAT TATAATTGCC TTTTGAATTC 300
 AGAAATTAAA ACCACTCCAC AGCTCGAG 328

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GAATTCGGCC TTCATGGCCT AATAAGGAAG AAATTGTCTC ACTTTATTGA ATAGTTGATT 60
 TAAATTTTCT GGTATTTAGA GGTAATATAG TATAAGTTTT TTGTATATTT ATCTAAGATT 120
 TTCCTTTTGA AAATTTTCTT CCCTTTTCAT ATTATTTTCA TTAACGATT TTCCTTTAAA 180
 ATTGTTACT AACAAGAACT ATCTAATATG CAATGAGATT TTTGCAGGGC ATTCTCGAG 239

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

```

GAATTCGGCC TTCATGGCCT AAGGAAAGTA CTTTAGACAA AAAAAAAAAA AAAAGTGAAA      60
TTAATTCCTG GGGCAATGAA AGGAAATGTC ATTGGCAGTT TTACCTTTAT TCTGCTAATG      120
GCTATTGTGT GTCTGTTTAC CTGGAGGCAC TTGGAACCTG TGGCACAGAA TGCTGTATGT      180
ACAGGATATC ATCTACATGG GAATAATTGT TGTAACACC CCAAACCTGA G                231

```

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

```

GAATTCGGCC TTCATGGCCT ACAATAGAGC TCTTAAACTT ATTTAACTGA AATTTGTAT      60
CTTTTCACCA ACATTTCCCC AACTCCCTT TACCCCACT ACTCCAGCCA CTGATAACCA      120
CCATTCTGTT CTCTATTCT TTTCTTTTT TTTTTTTTT TTTTAAAGAG ATGGCGTCTT      180
GCTGTGTCGC CCAGGCTGAA GGGCAGTGGC ATGATCTCGG CTTACTGCAA CCTCTGCCTC      240
CCCGGTTTAA GCAATTCTCT ACCTCAGCCT CCCGAGTAGC TGGGATTACA AGCACCCATC      300
CACTCGAG                                         308

```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

```

GAATTCTAGA CCTGCCTCGA GCCCTTTGTG GTTTTAAAGA AAAAAATTCT GTGCAGATCT      60
GTTCTCTCTC CTGCTCCTTC CCTTTTCTCT ACATACAGTG CTCATTGGAG GCTCCCCACT      120
CGAG                                         124

```

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

```

GAATTCGGCC TTCATGGCCT AATCGGTGTC TTTGGTAAAA ATTCTATGAG GATGACATAT      60
TCCATCATGT TATTCGTTTC ACATTTCCTT TTGCTCAGTC TCCAATGCAA GCACAGCTTG      120
TGGTATAACC TATTGTTTTT CCATTCTAAT AACTTCTCAA TCGATCTTCG TGTCTTTTA      180
CTGAGGCAAA TAACTGGCCA CATACTGCAA CCTAATGTGC AGCAGCAACA AAGGCAGCCA      240
CAAAGTAGCC AACGTACATT AACAGGAAGG TTCTTCTTAA GACAAGTGT AACTCTGTTG      300
ATGCTGGCTT TAAATTCCTC AGGAGCTACT TTTTCAGTTA ATGAAGAAGG GAATTCAGAT      360
TCAAATTTG                                     369

```

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

```

GAATTCGGCC TTCATGGCCT ACCGGCGAGG AATAGGAATC ATGGCGGCTG CGTGTTTCGT      60
GCTGCTGGGA TTCGCGCTGC TGGGCACCCA CGGAGCCTCC GGGGCTGCCG GCACAGTCTT      120
CACTACCGTA GAAGACCTTG GCTCCAAGAT ACTCCTCACC TGCTCCTTGA ATGACAGCGC      180
CACAGAGGTC ACAGGGCACC GCTGGCTGAA GGGGGGCGTG GTGCTGAAGG AGGATGCGCT      240
GCCCCGCCAG AAAACGGAGT TCAAGGTGGA CTCGGACGAC CAGTGGGGAG AGTACTCCTG      300
CGTCTTCCTC CCCGAGCCCA TGGGCACGGC CAACATCCAG CTCCACGGGC CTCCCAGAGT      360
GAAGGCTGTG AAGTCGTCAG AACGCATCCT CGAG                                     394

```

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

```

GAATTCGGCC TTCATGGCCT ACTGATGTTG AAGACGACAC CACGGCTTTG ATGGAATATC      60
AGATATTGAA AATGTCTCTC TGCTGTTCAT TCCTTCTGTT TCTCACACCT GGTATTTTAT      120
GCATTTGTCC TCTCCAATGT ATATGCACAG AGAGGCACAG GCATGTGGAC TGTTCAGGCA      180
GAAACTTGTC TACATTACCA TCTGGACTGC AAGAGAATAT TATACATTTA AACCTGTCTT      240
ATAACCACTT TACTGATCTG CATAACCAGT TAACCCAATA TACCAATCTG AGGACCCCTG      300
ACATTTCAAA CAACAGGCTT GAAAGCCTGC CTGCTCACTT ACCTCGGTCT CTGTGGAACA      360
TGTCTGCTGC TAACAACAAC ATTAACTTC TTGACAAATC TGATACTGCT TATCAGTGGA      420
ATCTTAAATA TCTGGATGTT TCTAAGAACA TGCTGGAATA GGTTGTCCTC ATTAATAAATA      480
CACTAAGAAG TCTCGAG                                     497

```

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

```

GAATTCGGCC TTCATGGCCT AACCAAAATCA ACAACAACCT ATTTAGCTGT TCCCCAACCT    60
TTTCCTCCGA CCCCCTAACA ACCCCCTCC TAATACTAAC TACCTGACTC CTACCCCTCA    120
CAATCATGGC AAGCCAACGC CACTTATCCA GTGAACCACT ATCAGGAAAA AAACCTCTACC    180
TCTCTATACT AATCTCCCTA CAAATCTCCT TAATTATAAC ATTCACAGCC ACAAACCTCG    240
AG                                                                                   242

```

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

```

GAATTCGGCC TTCATAGCCT ACCTAAATTA ATAATAATGT ATAGTTCAGA ATTGCTAAGA    60
GTACTTTTTT TTTTTTTTTT TNGAGACAGG TTCTCGCTCT GCCCTCCAGC CTGGTGACAG    120
AGCAAGATTG CATCTCAAAA AAGAAAAAAA ACACACAGCT AATAGAATTG CCATTGTTTT    180
TCATAATAGA ATCTAGCTGC TTAATCCAAC CTCACCTCGA G                                                                 221

```

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

```

GAATTCGGCC TTCATGGCCT AAAATCAAAG ACTTTGCCAA TACCATTCTT GGCCATGGAG    60
GCATCATGGA TCGCTTTGAC TGCCAGTATC TGATGGCCAC CTTTGTCAAT GTATACATCG    120
CCAGTTTTAT CAGAGGCCCT AACCCAAGCA AACTGATTCA GCAGTTCCTG ACTTTACGGC    180
CAGATCAGCA GCTCCACATC TTCAACACGC TGCGGTCTCA TCTGATCGAC AAAGGGATGC    240
TGACATCCAC CACAGAGGAC GAGTAGGGGC CACCCAGGGC CAGGAGAACA GGAACAGAAC    300
TGAGCAGGGG CAGGTCTCCA AGGCAAGCCC AGCTGGTGTG ACTTAGACAA TGACGAGGCT    360
TCAACTCACT GTCTTTTTTT TTTTTTTTGG GAGGGTATTT TTTATTTGTG GGTTCAAAAA    420
ATCTGTATAT ACAGTCTATG TGTTTAGAAT TTGTGTTGTA AGTAAACTAC AGCTTTGAGT    480
TGGAAGAAG TCACGGGTTG TAAAACCAT TGGATTTTTT TAAAACAAAA GTATTAATAA    540
TCTGGAAGAC TCGAG                                                                                   555

```

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

GGCCGATCAG GTTATTTTTT GAAAGTTTTA CTTACAGAGC ATATAAATTA CCCTTGGTTA	60
TTCTCAGCTG TGATTGAGTT CTGTGAAAGC ATAGTACCCT AGTACCCTGG GATATCTCTA	120
CATGTGAAAT TATTCAAATG TCTCCCTTAC TTTTTTTTTT TTTTTTTTTG AGACAGGCTC	180
TGTTGCCCAT GCTGCAGTGC AGTGGCACAA CTATGGCTCA TCTCAGCCTC GACCTCCTGG	240
GCTCAAGCGA TCCTCCCACC TCAGCCCCC AGGCAGCTGG GACCACAGGC ACACACCACC	300
ATGTCCAGCC AATTCCTGTA TTTT	324

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

GAATTCGGCC TTCATGGCCT AGTGCCGGGG AGAAAGGGCT TCCTCCCCCA CACATCAGAC	60
AGGGCACCAA TGAGTGGGGC ACTCAAAAAA GAGAGCAGGC CCTGGAGAGG AAACCAAAGC	120
AAAGGTTAGT TTTATAATCT GATCCCTCAA TTACCTGTAA TTCATATTTT CTAAATGCAT	180
TAGCTCTAAT TCATTGTACT GCCCCCAAAA CAGAATAATA CTTTGAAACA TTAAATACAA	240
ACTACAATA AAAAAATAAA ATTAGGCCTG GCGTGGTGGC TCATGCCTGT AATCCCAGCA	300
CTTTGGAAGG CCGAGGCGGG TGGATCACTC GAG	333

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GAATTCGGCC TTCATGGCCT AATTTGAATC AACACAACCA CCCACAGCCT AATTATTAGC	60
ATCATCCCTC TACTATTTT TAACCAAATC AACACAACC TATTTAGCTG TTCCCAACC	120
TTTTCTCCG ACCCCCTAAC AACCCCTC CTAATACTAA CTACCTGACT CCTACCCCTC	180
ACAATCATGG CAAGCCAACG CCACTTATCC AGTGAACCAC TATCAGGAAA AAAACTCTAC	240
CTCTCTATAC TAATCTCCCT ACAAATCTCC TTAATTATAA CATTACAAC CACAGAACTC	300
GAG	303

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GAATTCGGCC	TTCATGGCCT	AGGGATTAA	AGAGTTTTTC	TTGGGTGTTT	GTCAAACCTT	60
TATTCCTCT	CTGTGTGCAG	AGGGGATTCA	ACTTCAATTT	TTCTGCACTG	GCTCTGGGTC	120
CAGCCCCCTTA	CTTAAAGATC	TGAAAGCAT	GAAGACTGGG	CTTTTTTTCC	TATGTCTCTT	180
GGGAACTGCA	GCTGCAATCC	CGACAAATGC	AAGATTATTA	TCTGATCATT	CCAAACCAAC	240
TGCTGAAACG	GTAGCACCTC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

GAATTCGGCC	TTCATGGCCT	ACCAACAGCA	AGCTCCAATA	TCACACATCC	AGACTCCTAT	60
GCTTTCCCAA	GAACAGGCAC	AACCCCGCA	GCAGGGTTTA	TTTCAGCCTC	AGGTGGCCCT	120
GGGTCCCTT	CCACCTAATC	CAATGCCTCA	AAGCCAACAA	GGAACCATGT	TCCAGTCACA	180
GCACTCAATA	GTTGCCATGC	AGAGTAACTC	TCCATCCCAG	GAACAGCAGC	AGCAGCAGCA	240
ACAGCAGCAG	CAACAGCAGC	AGCAACAACA	ACAGAGCATT	TTATTCAGTA	ATCAGAATAC	300
CATGGCTACA	ATGGCGTCTC	CAAAGCAACC	ACCACCAAAC	ATGATATTCA	ACCCAAATCA	360
AAATCCAATG	GCTAATCAGG	AGCAACAGAA	CCAGTCAATT	TTTCACCAAC	AAAGTAACAG	420
TCTCGAG						427

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

CGATTGAATT	CTTGCTGTGTT	CTGCCTCACT	CCCGAGCTCT	ACTGACTCCC	AACAGAGCGC	60
CCAAGAAGAA	AATGGCCATA	AGTGGAGTCC	CTGTGCTAGG	ATTTTTCATC	ATAGCTGTGC	120
TGATGAGCGC	TCAGGAATCA	TGGGCTATCA	AAGAAGAACA	TGTGATCATC	CAGGCCGAGT	180
TCTATCTGAA	TCCTGACCAA	TCAGGCGACT	TTATGTTTGA	CTTTGATGGT	GATGAGATTT	240
TCCATGTGGA	TATGGCAAAG	AAGGAGGGTC	TCGAG			275

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GAATTCGGCC	TTCATGGCCT	ACGTAATTCT	GGAAAAGTGA	ATACTTGTGA	AGAGTCGTCT	60
TGAATGATTT	GTAAAAAATC	CTGTTCTTAT	ATTCACGAG	TTTCGAATCT	TTGTCAGAGG	120

```

AGTATTACCA TTAGATTGAA AAAAAGGAAA ATAAATAATA AACACTTTTA AAAAACTCC      180
CCATTCTCTT ATTCTCACTT TTAGGAAAAG AGACTGACTA ATATCTTCTG CCACAAATAC      240
CGATGTTCTT AAAAATATTT ATGGGACTGC TTTTGCCAAC CAGCCCTATT TIGTTTTCAT      300
ATCCCTTTTT GTCCTCATCT TTCCAACTC ATAAACTCGA G                          341

```

(2) INFORMATION FOR SEQ ID NO:768:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

```

GAATTCGGCC TTCATGGCCT ACAGAAAGAG TTTGAGACCT GAATAGCTCC CAGATTTTCAG      60
TCTTTTCCTG TTTTGTGTTA CTTTGGGTGA AAAAAAAAAA AAGTCTGATT GGTTTTAATT      120
GAAGGAAAGA TTTGTAATAC AGTTCTTTTG TTGTAAAGAG TTGTGTTGTT CTTTCCCCC      180
AAAGTGTTT CAGCAATATT TAAGGAGATG TAAGAGCTTT ACAAAGAC ACTTGATACT      240
TGTTTTCAAA CCAGTATACA AGATAAGCTT CCAGGCTCGA G                          281

```

(2) INFORMATION FOR SEQ ID NO:769:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

```

GAATTCGGCC TTCATGGCCT ACTAACGAGG AAAGGGATT AAAGAGTTT TCTTGGGTGT      60
TTGTCAAAC TTTATCCCT GTCTGTGTC AGAGGGGATT CAACCTCAAT TTTCTGCAG      120
TGGCTCTGGG TCCAGCCCCT TACTTAAAGA TCTGGAAAGC ATGAAGACTG GGCTTTTTT      180
CCTATGTCTC TTGGGAACTG CAGCTGCAAT CCGACAAAT GCAAGATTAT TATCTGATCA      240
TTCCAAACCA ACTGCTGAAA CGGTAGCACC TGACAACACT GCAATCCCCA GTTTAAGGGC      300
TGAAGCTGAA GAAATGAAA AAGAAACAGC AGTATCCACA GAGAGACTCG AG              352

```

(2) INFORMATION FOR SEQ ID NO:770:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

```

GAGCGTGGTG GATATAAAC AGGTAAGAGA CTTTCATGGT ATACCTTTAT ATTGTTGGAT      60
TAAAGGCACT GCCAACTCAA AAACTTAAC CGAAAATTTT TTTTAATCAG TTAAATATTT      120
ACTGATATGA AAATGACATG AACTTAACCT TTTGTGTTT ACTTAAAGGG TGCTCTGTTT      180
GAACTTCCT CAGACAACTG AATGGGAGAA CCAGATGAAT TTAGTAAAG TATTAACGTC      240
AAATATTTAT ACTGCTTTT TTTGTTGTT TGTTTTGGAG ACAGAATCTT GCTCTGTTGC      300

```

CCAGGCTGGT CTCGAG

316

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

```

GAATTCGGCC TTCATGGCCT ACTTTGATGG AATATCAGAT ATTGAAAATG TCTCTCTGCC      60
TGTTTCATCCT TCTGTTTCTC ACACCTGGTA TTTTATGCAT TTGTCCTCTC CAATGTATAT      120
GCACAGAGAG GCACAGGCAT GTGGACTGTT CAGGCAGAAA CTTGTCTACA TTACCATCTG      180
GACTGCAAGA GAATATTATA CATTTAAACC TGTCTTATAA CCACTTTACT GATCTGCATA      240
ACCAAGTTAAC CCAATATACC AATCTGAGGA CCCTGGACAT TTCAAACAAC AGGCTTGAAA      300
GCCTGCCTGC TCACTTACCT CGGTCTCTGT GGAACATGTC TGCTGCTAAC AACAACTTA      360
AACTTCTTGA CAAATCTGAT ACTGCTTATC AGTGAATCT TAAATATCTG GATGTTTCTA      420
AGAACATGCT GGAAAAGGTT GTCCTCATTA AAAATACACT AAGAAGTCTC GAG              473

```

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

```

ATACAGTAAT CAAAGTAAGT AATATTTCAT TCCAATATTT TTAATAATCA GAATTAATGC      60
AAAAAAAACC ATGATGAACA AAATATTAAA ATTTAAATAA AAGACAGGAT TAGTATTACT      120
GAGTTTTCCT TTGTGCCAG GCTCTAATAT GGCTTGGCAT GGGGCAGAAC ATTACAACAT      180
ACCAAGTCGTG TCATGGTGCC CAAGGCTCCA CAGACCTCAG TGGCTCCCTG CTGCCTGCCA      240
CAGCAATCTC GAG              253

```

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

```

GAATTCGGCC TTCATGGCCT AGTGAGAATT GACTGTTGCT TTGTTTGCC TGCTTACTGT      60
TTTCTTTTAT TTATTGTTT TTGGACCTGT GGCACAAAGG ATCTGTTTAC TGACCATCCT      120
TATTGTGAGG CACACAGTCA CCATGGCACC CTGCGCGTTA CTCCTGTTCC ACTTGTTTAT      180
TCTCTGTATC CCCATACTAG TTATTATCGA AACCATCAGC CTACTCATTC AACCAATAGC      240
CCTGGCCGTA CGCCTAACCG CTAACATTAC TACAGGCCAC CTGAG              286

```

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

```

GAGGCTGACA AAATACTCAC CTTTACCTT ATTTTTCAT TTTATACTCA CAACCATATT      60
TTTTTGGCC CCCTTCCCTT TATTTAACT CATAACTGAT ACTTAAAGGT GCTCTGCCTT      120
ATTAAATCAG CTCCTAGGCT GCAAGTGCAT AATATTTAAA AATTGCAAC TTTGACTTTT      180
TAAAAATCTG GTCTTGGTAT GGAGCAACTT TGCCTTTTTT TTTTNTTTT TTGAGACAGA      240
GTCTCGCTTT NTCGCCCAGG CTGGAGTGCA GTGGTCCCAT CTCAGCTCAC TGCAACCTCC      300
TCCTCCGGG TTCAAGAGAT TCTCTGCCT CAGCCTCCG AGTAGCTGGG ATTACAGGTG      360
CCTGCCCAA CACCCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

```

GGCCTGGTAG GATAAGAATA TAACTTCAG GGTGACCGAA AAATCAGAAT AGGTGTTGGT      60
ATAGAATGGG GTCTCCTCCT CCGCGGGGT CGAAGAAGGT GGTGTGAGG TTGCGGTCTG      120
TTAGTAGTAT AGTGATGCCA GCAGCTAGGA CTGGGAGAGA TAGGAGAAGT AGGACTGCTG      180
TGATTAGGAC GGATCAGACG AAGAGGGGCG TTTGGTATTG GGTATGGCA GGGGGTTTTA      240
TATTGATAAT TGTTGTGATG AAATTGATGG CCCCTAAGAT AGAGGAGACA CCTGCTAGGT      300
GTAAGGAGAA GATGGTTAGG TCTACGGAGG CTCCAGGGAA GCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

```

GAATTCGGCC TTCATGGCCT AAGAGGATAA GGGAAGAAAA AGAAGAAAGT ATTCCATTCC      60
CACATCCCTT TAGGTGGCT TCTTATTTTA TGTTTTGTT GGTGTGTTTA TTTTGCTTTG      120
TTAACATTTT CAACTAGCTA TAGAAACGTT TGCAATTCTT ATTACTGATT AGCATTCCAA      180
AACTTTGTAA TGAACATTTT TCTCTCTTTC TTTTTTTTTT TTTTITNGAG ACAGGGTCTC      240
GCTCTGTAC CAAGCTGGAG TGCAGTGAGC CAAGATCCTA CTGCTGTCCA TTCCAGCCTG      300
GGTGACAGAA CAAGACCTTG TCCGCCACC TTCCACCCCC CCCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

```

GAATTCGGCC TTCATGGCCT ACATGTTTAT TGAGCATTTA CTGTTTACCC ATCAGTATTC      60
TTGATGCTAA GGATATAGCA GTGAACAAAA CAATCCTTGT GGACTTACAT CATAGTAGGG      120
AAAATAGACA ATAAATAAAT GTATGATAAG TCAGTTGATA ATAAGTGCTA CGAAGTAAAA      180
CAAAGCAGGA ATAAAGTTGG GGAGAAAAGT GGAGGGTGAT TGCTATTTC A GTTGAGATCA      240
TTGGGATGGT CTTTCTGAG GAGGGGACAT TTGCATAGAG AAGCAAGGAT GTGAGTTATG      300
TGTCTGCTGT GTGTAGAACA TTCTGGGAAA GGCAGAGAA GGAACAAGA CTATTCCAGA      360
AAAAGAGGGC ACTCGAG                                     377

```

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

```

GAATTCGGCC TTCATGGCCT AGCACAGCTA GACGGTTCCA GCTCAGGGTC TCTCATGAAG      60
TTGCAATCAA AATATTGGCA GGAGAGAAAA ACATATTTTC AGAAGCTGCA GGCATAGGAA      120
GACTTGGCTG GGGTTGAAGG ATCCACTTCC AAGATGGCGC ACTCAGTGGC TCTTGGCTGG      180
AGGCCTCAGT TCCCTGCTGC GTGGAGCTCT CCCTCCAGCT GCTTGAGTGG ACTCATGACA      240
TGACAGTGGC CTCCCCTGGA GCAGTCGATC CAACAATGAG CATGGCCATG AACTAGAGCT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

```

GAATTCGGCC TTCATGGCCT AGCCAAAACC ACAGAATATA TAATATAGAT CTTGGGGATA      60
CAGCAGAGAA AAAAGACAAA AATCCCTGTT ACAATCCGTT CTAGAATTGA TGTTCCTTTG      120
TTGGTTAATT CAAGTTTGA TTTCAGAAAT CTTACCTCTT GGTGACTGCC TAGAGTGGA      180
TTGGGCTGGA GGGGAGGAAC TGTTCATGTT GGAAATGGGG AATGGGCCAA AAATGCAATT      240
GAGTAGGTTG ATTAAGTGT CTGCTGTCAG AGTGAAGCA GGGGTAGTTT CCCTTCCGA      300
CCAGAGGCAT CTCGAG                                     316

```

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

```
GAATTCGGCC TTCATGGCCT ACAGAAGATT TGGACAATTC CATTGATAAA ACAGAAGCTG    60
GAATTAAGGA GCTTCAGAAG AGTATGGAGC GCTGGAAAAA TATGGAAAAA GAACATATGG    120
ATGCTATAAA TCATGATACT AAAGAACTGG AAAAGATGAC AAATCGGCAA GGCATGCTAT    180
TNAAGAAGAA AGAAGAGTGT ATGAAGAAAA TTCGAGAACT TGGATCACTT CCCCAGGAAG    240
CATTGAAAA GCACCAGGCT CGAG                                         264
```

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

```
GAATTCGGCC AAAGAGGCCT AGCGATTGGG TCTTTGATAT CTGTAAGCCG TTGAATTAGC    60
CCTGCCCTCT GTTCTTAGTT TAGGAGACCA TAGATGTGCC CTTATTATTG AAACGTATTT    120
TATTCAGTTA CTGAAGTTAT CTTACCTGAT ACATAATTTT ACCCATAGAA AATAATATGA    180
AAATAGCAAA ATCACTCAGG TAAGATAGAT GAGTGCCTGC TGTGTTCAAG AGACTGTTAA    240
TATGAGGCTC TGGGGCTGCA AAAAATCAAG TTGCTAAGAA ATATGAGGTC AGAGCAGCAG    300
AAGTTCTGAG TAACCACTGA TTA CTGGACT TGGGGTGATC AGAAGTGACT GTGTGGGAGA    360
GGTGAAATTG AGCAGACTCT GAAGGAACCT CTGGGTTTTG GTAAATAGGG AGCTGGGGAT    420
GAGGATGCCC CAGGTTTTAG AAAGAACACA GGCTGTTGAA TCACACCTGG GTTCAAACCC    480
TGGCTTGCTA CTCCTAGTT TGTGACCTTG TCAAATTCCT TGATTTCTTT TTTCTTTTTC    540
TTTTTTTAAT TTTGGAGACA ACAGTCTCGC TCTGTCACCC                    580
```

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

```
GAATTCGGCC AAAGAGGCCT AGAATGGTAG AGTAAAAAGA ACCCTCTGCT GAGTAACCAA    60
GCCTTTAATT TCCTGTTCTT GCTGTAGGGC TTTACAAAT GCATTTTTC GCGGTTGGT    120
GTGTCCTCGA G                                         131
```

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GAATTCGGCC AAAGAGGCCT AGATTGAGGT TGTGGTAGAT TAGGCGTAGG TAGAAGTAGA	60
GGTTAAGGAG GGTGATGGTG GCTATGATGG TCGGCTCGA GGCAGGTCTA GAATTCAATC	120
G	121

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GAATTCGGCC AAAGAGGCCT AAGCAAGATG AAGCCCAACA TCATCTTTGT ACTTCCCTG	60
CTCCTCATCT TGGAGAAGCA AGCAGCTGTG ATGGGACAAA AAGGTGGATC AAAAGGCCGA	120
TTACCAAGTG AATTTTCCCA ATTTCCACAC GGACAAAAGG GCCAGCACTA TTCTGGACAA	180
AAAGGCAAGC AACAACTGA ATCCAAAGGC AGTTTCTTA TTCAATACAC ATATCATGTA	240
GATGCCAATG ATCATGACCA GACCCGAAAA AGTCAGCAAT ATGATTTGAA TGCCCTACAT	300
AAGACGACAA AATCACAACG ACATCTAGGT GGAAGTCAAC AACTGCTCCA TAATAACAA	360
GAAGGCAGAG ACCATGATAA ATCAAAGGT CATTTTCA GGGTA	405

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GAATTCGGCC AAAGAGGCCT ACTACTCACC TCTTGCTCTC TCCCAACCAT AGAAACAGCC	60
ACGACTCCTA CCACAACTT GGGAAACACC ACCACTGAGA CCACCTCCCA CAGTACTCCC	120
AGCTTCACTT CTTCAGCCAT CTAATCCACC GTCAACATAT CCACAACTAC CATCTCCTCA	180
TTTCCCCCTT CCTCAGGTAC CATGGTGACA TTCACAACCA TGAACCCATC CTCTCTGAGT	240
ACAGACATAT CTACCACCAC ACTGAAAAAT ATCACCACGC CTTCTGTGGG CTCTACTGGT	300
TTCTGACTG CAGCTACAGA CTTCACTCA ACATTCACTG TTTCCACTTC CTCAGCAATG	360
TCCACAAGTG TCACTCCATC TGCCCCCAGC ATCCAGAATA AAGAAATCTC AACACTTGTG	420
AGTACAACCA CTACCACCAG TCCCACTGAG AGAATGACTC TCACAAGTAC AGAGAATACC	480
CCGACAAGTT ACATCCTGAC CACCACTCCA GTGACATATT CATTTTCCCC TTCCATGTCT	540
GCCAGCAGTG ACTGGACCAC TGACACAGAG AGCATCTCCT CAGCTCCAGC CATCACCAGT	600
ACACTCCACA CAACAGCTGA ATCCACCCTG GCAGGTCTAG AA	642

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAATTCGGCC AAAGAGGCCT ATGGCCTTGG AAGGGATGAG CAAACGGAAG AGAAAGAGAA	60
GTGTCCAGGA GGGAGAGAAT CCTGACGACG GCGTTCGCGG GAGTCCGCCG GAAGACTACA	120
GGCTTGGACA GGTCGCCAGT AGCTTATTTT GCGGCGAACA CCATTCCAGA GGTGGCACCG	180
GTCGGCTGGC GTCCCTCTTC AGTTCTCTGG AGCCCCAGAT TCAACCCGTG TACGTGCCTG	240
TGCCTAAACA AACCATCAAA AAAACGAAAC GGAATGAGGA GGAAGAAAGT ACATCCCAGA	300
TTGAAAGACC ACTTTCGCAA GAACCTGCCA AAAAAAGTGA AGCGAAGAAG AAACACACTA	360
ACGCAGAAAA AAAGTTGGCA GACAGGGAAA GCGCTCTAGC GAGTGTCTGAT TTAGAAGAAG	420
AAATTCACCA GAAACAAGGG CTTAGCTCGA GCAGGTCTAG AATTCATG	469

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCGGCC AAAGAGGCCT AAGAAAAGAT ATAAATCAGA GAAAAAGCAT GAAGCGTATC	60
ATATTGATTT TAACAGTATT GCTTGCCATG TTAGGGCAGG TTGCCTATGC GCAGAAAACG	120
TGTGTCATCG CATCGGCAGA AAATCATGTG CCTATTCGTG AAGCACTTAT TCATACCAAT	180
AACAATCATT GGGCAAGAAC AGATTATCGG GGCTATTGGA CGATGCGCTA TCAGTTTGAT	240
TCAGCAACCG TATCGAAACC TGGTTTATG AAGGCAACTA TCCGGTACAA GGAAGTCCG	300
GATACTCTGT TTCTCTTGCC GGATGCCAAA CAGTTAGGCG AAGTGACAGT TTGGGGCAAG	360
AATCAGGAAG GCATCAAAAA TATGGAAGAG GATATTCAGG AGAAGATAAA CTCTTTGCCA	420
ACTTCATCTG CTGGCATTGG TTTTGATGCT TTCGGATGGA TGGATAAACA GGGAAAACGT	480
GATAAGAAGC ATCTGCAACA G	501

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

TGATGATCGA TATCCAGAAA GACACTGCGG TGAAGGTGA GGAGATTGAA GTCAACTGCA	60
CTGCTATGGC CAGCAAGCCA GCCACGACTA TCAGGTGGTT CAAAGGGAAC GCAGAACTGC	120
AG	122

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GGTGAGCTGA GATCGACCA CTGCACTGCA AGACCCTGTC TCAAAACAAA CAAACAAACA	60
ACAACAACAA CAACAACCA AACCAACAA AAAACCTGCA TAGCCAATA GACCAGCATA	120
GAGGGCGAAA ACCATGCTTT TTGTCAAATG GTACTGTTTA TTCTGTTTTG CTGTCAGCTG	180
GTTTGCCGCT TCTGATAAAG CTAGCCCTTG CTGTGTGCAT GCAGGTTATA GTGCCCAGGC	240
TCATATTTCC TCTTCTGCT GCACCTCACT CGAG	274

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GAATTCGGCC TTCATGGCCT AGGGAAAGGA GCGGCAGCC AGGCTGTGTC CCCTGACCGT	60
TGGAGCGTCT GCGACCCCG CATCCCGCA CCCTCAAGGC ACCTCCAAAG ATGATGATGG	120
GTTGTGGGGA GTCAGAGCTG AAGTCGGCGG ACGGGGAAGA AGCCGCGGCG GTCCCGGGGC	180
CACCCCGGA GCCCAAGTC CCGCAACCG	209

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GAGAGAATTA AAGAGAACCA CNAAGCTGAA CCTCAAAAAG TTAGCCTGGC GAGGGGAGGA	60
TGATGAGATT TCCCCTGTTG TCACATAAAC AAGGAAGTAA AGGGGGCCCC TTGTGCTCTC	120
AGAACTCCAA GCATGAAACG ATAGCAAAGG GAAAAACAGC TAAGTGTTTC CTGGCTGAAT	180
TTTATTTTGC TTTCAGTTTC TGCCATTTC GTTCCTGTGA TCGTGCTTTG AGGTGCACTG	240
AACTGCAGCA AACCCAGGGG ATCCAAGGCT ACGTTGAAAA GCCTTTGACC ACAGTGCAGG	300
GAGCAGAAGA CATTAAATGAC GTGATGTCGA CACAGCCCGC ACTCAGGATC CTCCAGGAAA	360
AGAACACAGA GATAACCCCG GAACTCGAG	389

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

```

GTGCTTTGGA TTTTGCATCC AGCTTTTTCT CAACACCCCC GCTGGAATC AGCGGCTCCA    60
TCTCTTCGCC TTCGGAAGCA CCTGCCGTCTC TGTCTCTGAT GCCGAGTGAC TTGTCCCCT    120
TCACATCTCA GTCTTTTCT CCCTTGGTTG AGACATTTAC ATTGTTTGAC TCTAGTGATC    180
TGCAGTCATC TCAGCTGTCT CTTCCAGTT CCACAAATCT TGAGTTTTCC CAGCTCCAGC    240
CAAGTTCCGA GCTGCCTTTA AACACCATCA TGTGCTACC TACCCTTCT GAGGTGTCAC    300
CATGGTCAAG CTTCCCTTCT GATTCTCTCG AG                                332

```

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

```

GAATTCGGCC TTCATGGCCT ACTGGAATTT CTTTCTTGCC CTTTCATATT TTAAGATGGC    60
TGGAAATAGCA CAGGGAGTAT ATAGCAGATA TCTTCTGGA AATAATTCAT CTGAGGATGC    120
CTTTTATTTT GCCAATATTG TGCAACCTCT GGCAGAACT GGACTACAAC TCTCCAAACG    180
AACTTTCAGT ACTGTACTAC CACAGATTGA TACTACTGGA CAGTTGTTTG TACAGACTCG    240
GAAAGGTCAG GAAGTTCTCG AG                                262

```

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

```

GAATTCGGCC TTCATGGCCT ACTATGCCGT CATGATAGAG AAGATGATCC TGAGAGACCT    60
GTGCCGTTTC ATGTTTGTCT ACGTCGTCTT CTTGTTCCGG TTTTCCACAG CGGTGGTGAC    120
GCTGATTGAA GACGGGAAGA ATGACTCCCT GCCGTCTGAG TCCACGTCGC ACAGGTGGCG    180
GGGGCCTGCC TGCAGGCCCC CCGATAGCTC CTACAACAGC CTGTACTCCA CCTGCCTGGA    240
GCTGTTCAAG TTCACCATCG GCATGGGCGA CCTGGAGTTC ACTGAGAACC ATGAACTTCT    300
CGAG                                304

```

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GCGATTGAAT TCTAGACCTG CCTCCAAGCA GCTGCAGTAT CTCGGAAGAA AAAACGAAGA	60
ATGGGAACCT ATAGCCTGGT TCCTAAGAAA AAGACCAAAG TATTAAACA GAGGACGGTG	120
ATTGAGATGT TTAAGAGCAT AACTCATTCC ACTGTGGGT CCAAGGGGA GAAGGACCTG	180
GGGCCAGCA GCCTGCACGT GAATGGGGAG AGCCTGGAGA TGGACTCAGA TGAGGACGAC	240
TCAGAGGAGC TCGAG	255

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

CTAGTCTTCC AACCTTCTG GACTTCTTT GCTCTGTCT TGTTTGGGT GTACTGGATC	60
ATGACACTTC TTTTCTTGG CACTACCGGC AGTCTGTTC AGAATGAGCA AGGCTTTGTG	120
GAGTTCAAAA TTTCTGGGCC TCTGCAGTAC ATGTGGTGGT ACCATGTGGT GGGCCTGATT	180
TGGATCAGTG AATTTATTCT AGCATGTGAG CAGATGACAG TGGCAGGAGC TGTGGTAACA	240
TACTATTTTA CTAGGGAAGT ACTCGAG	267

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GAATTCGGCC TTCATGGCCT AGGGGGAGTT TAGCTGAAAC AAGTTTTACA GAAGCAGAGC	60
TGGCAAATAG TTAAATATT AATTGGTTAC AATAGCAGTT ACAAACAAA TAAACAGTTC	120
CAGGTGCAGG GGCTTAACT ATCACAAAGA GAGAAATGCA GGGGTTTTGC GTGACATTCA	180
CCGAG	185

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

GGGCGTGTGA CGACTGCTGG GAGAGGAAAG CGAGACATCA TTCCAACCCT CCAGAAGCTA	60
AAGATCCTGG AACTCAAGGG GAAACTAAG GTAAGTGCGA AAGCGAACAA GCAAACATGT	120
CCTCAACGGG GCAGGCAGGC TGTCGGGGTA CAGAGCTGGG ATCTGGGAAG GAACAGAGAG	180
GGCCGCTCAG GGAGAGGAAG CACAGTGCCA CCGGAGGCAC GCACTCAGCA GGCCTCGCA	240
GGCTGGGCAG AGGTAGAGAA GCAGCGCTGC ACAGGCAGGC AGCTGACCCA GGGCTCTTAG	300

AGCCGGGCAG GAGAGCTGGT GTGGGACCTG GGAGGAGGAC AGGAGCCTTC AAAGCAGCAC 360
 CGCCTGATTG CAGCCAGGAG GGTAGCATCA AGGAAGATGG AACTGCGGCC AGGCCACATC 420
 CAGGGGTGCT CGAG 434

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GAAAAGTCGG ATGCTGGCCT CTGGAAATCA GCCAGATCAA GATATTACAC ATTTCTTCCA 60
 ACAGATCCAG GAGCTCAATT TGGAAATGGA AGACCAACAG GAGAACCCTAG ATACTCTTGA 120
 GCACCTGGTC ACTGAACTGA GCTCTTGTGG CTTTGGCGTG GACTTGTGCC AGCATCAGGA 180
 CAGGGTACAG AATCTAAGAA AAGACTTCAC AGAGCTACAG AAGACAGTTA AAGAGAGAGA 240
 GAAAGATGCA TCATCTTGCC AGGAACAGTT GGATGAATTC CGGAAGCTGG TCAGGACCTT 300
 CCAGAAATGG TTGAAAGAAA CTGAAGGGAG TATTCCACCT ACGGAACTT CTATGAGTGC 360
 TAAAGAGTTA GAAAAGCAGA TTGAACACCT GAAGAGTCTA CTAGATGACT GGGCAAGTCT 420
 CGAG 424

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

GAATTCGGCC TTCATGGCCT AGGGGTGCTG TGTGTTTTTC AGGGCGCCCT GCGTCCGGCA 60
 GAGGAGGCGA GCATCCCGCT CAGGTGATGA GGAACCCCTC GCGCACCCAG CGCAGAAGGC 120
 TGCTGCCGCC GGACGCCTCC ATTGTTTAC CACAACAAGG GCCGGATTCT CACCCAGCAG 180
 GATCCTAAGG CCTTTGTAGT CCTTCAGCCA CTGTGGGCC TGCCTCTGCC TGTCTTCTG 240
 GAATGTCTTG GGGGTTTGA TCCTGTCACT GTGACCTGCA AATCCAAGAG ACAACTCGAG 300

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GAGAAATCAG TGAAGGATTT GCAACGCTGC ACCGTTTCTC TAACTAGATA TCGCGTCATG 60
 ATTAAGGAAG AAGTGGATAG TTCCGTGAAG AAGATCAAAG CTGCCITTGC TGAATTACAC 120
 AACTGCATCA TTGACAAAGA AGTTTCATTA ATGGCAGAAA TGGATAAAGT TAAAGAAGAA 180
 GCCATGGAAA TCCTGACTGC TCGTCAGAAG AAAGCAGAAG AACTAAAGAG ACTCACTGAC 240

CTTGCCAGTC AGATGGCAGA GATGCAGCTG GCCGAAGTCA GGGCAGAAAT TAAGCACGGT 300
CTCGAG 306

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

GCTCGCGGCC GTTCAGAATT ATAAGGCTGT CTGCAGAGAT TTGAAAAATG GCAACAAATG 60
AAAGTGTGAG CATCTTTAGT TCAGCATCCT TGGCTGTGGA ATATGTAGAT TCACTTTTAC 120
CTGAGAATCC TCTGCAAGAA CCATTTAAAA ATGCTTGGAA CTATATGTTG AATAATTATA 180
CAAAGTTCCA GATTGCAACA TGGGGATCCC TTATAGTTCA TGAAGCCCTT TATTTCTTAT 240
TCTGTTTACC TGGATGTCTC GAG 263

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GAATTCGGCC TTCATGGCCT AAATAGTTAG TCACCTTCTG ACCTTCTCCT CTTTCTCAAA 60
GCCTTCTGTC CCTGGTTTTT GCAAGTGCTG CATTTCCGCC GAGAATCCGC GTTGCCTACT 120
GCTGCCACCT CCTGTTTATT TAGAACTATG CAAAGACTCC GCTTCCGTTT TCCTGAGCTC 180
CTCGGGCCCC AGAGTCTCTG TTTGATTATT TATTTATTTA TTTATTTATT TGCCAAAAAT 240
TCTCTCTTTC AACTTATAGA ATGCACCCAA CTCGAG 276

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

GAATTCGGCC TTCATGCCTA CAGCCATATT AAACTAAGT AAAGTCTGCC CTGGGAAGTA 60
CACTTTTCAGC TTGACTGTAG TAGACTCTGA TGGAGCTACC AACTCTACTA CTGCAACCT 120
GACAGTGAAC AAAGCTGTGG ATTACCCCCC TGTGGCCAAC GCAGGCCCCA ACCAAGTGAT 180
CACCCTGCCC CAAAAGTCCA TCACCTCTTT TGGGAACAG AGCACTGATG ATCATGGCAT 240
CACCAGCTAT GAGTGGTCAC TCAGCCCAAG CAGCAAAGGG AAAGTGGTGG AGATGCAGGG 300
TGTTAGAACA CCAACCTTAC AGCTCTCTGC GATGCAAGAA GGAGACTACA CTTACCAGCT 360
CACAGTGACT GACACAATAG GACAGCAGGC CACTGCTCAA GTGACTGTTA TTGTGCAACC 420
TGAAAAAAT AAGCCTCCTC AGGCAGATGC AGGCCAGAT AAAGAGCTGA CCCTTCCTGT 480

GGATAGCACA ACCCTGGATG GCAGCAAGAG CTCAGATGAT CAGAAAATTA TCTCATATCT 540
 CTGGGAAAAA ACACAGGGAC CTGATGGGGT GCAGCTCGAG 580

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

CAAATTGATT TCGGCACAGT TCTGGGAGCT GGGACATTCA AGGTCACCAC GTTGCCACCT 60
 GTGAAGGCCT TCTGCTGCAT CCTCATGTTG GGAAGATCA GAAGTGAGAA CACATGCTGG 120
 CCAGTCCTTT CACAGCAGCA TCAATCCGTG CATGGGGCAG GGCCCTCGGC CTGAGCGCCT 180
 CCCCAGGCC CTAATCCCA GCACTGCCCT GCTGGGGATG GAATTTCCAA CATGAATCTG 240
 GGGGATGCTT TCGGACCACA GCCGGGGAGC CTGCCCTGGC TTCCAGCTGC TGGTGGCCCA 300
 GGGGCTCCCT GGCTTGCCCTC GAG 323

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

GCGATTGAAT TCTAGACCTG CCATTCTCGC TCTGCCGACG TTGACTCTCT CTCTGAATCC 60
 AGTCCCAACT CCAGCCCTGG CCCCTGTCCT GAGAAGGGCC CACCACCCCA GAAGCCGAGC 120
 CATCTCCCAG GGGGCCCTCA TCGCCATCGT CTGCAACGGT CTCGTGGGCT TCTTGCTGCT 180
 GCTGCTCTGG GTCATCCTCT GCTGGGCTG CCATTCTCGC TCTGCCGACG TTGACTCTCT 240
 CTCTGAATCC AGTCCCAACT CCAGCCCTGG CCCCTGTCCT GAGAAGGGCC CACCACCACT 300
 CGAG 304

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

GAATTCGGCC TTCATGGCCT AGATATGAGA AATGAGTGTG GGACGTCGAA GAATAAAGTT 60
 GTTGGGTATC CTGATGATGG CAAATGTCTT CATTATTTT ATTATGGAAG TCTCCAAAG 120
 CAGTAGCCAA GAAAAAATG GAAAAGGGGA AGTAATAATA CCCAAAGAGA AGTTCTGGAA 180
 GATATCTACC CCTCCGAGG CATACTGGAA CCGAGAGCAA GAGAAGCTGA ACCGGCAGTA 240
 CAACCCCATC CTGAGCATGC TGACCAACCA GACGGGGGAG GCGGGCAGGC TCTCCAATAT 300
 AAGCCATCTG AACTACTGCG AACCTGACCT GAGGGTCACG TCGGTGGTTA CGGGTTTTAA 360

CAACTTGCCG	GACAGATTTA	AAGACTTTCT	GCTGTATTTG	AGATGCCGCA	ATTATTCACT	420
GCTTATAGAT	CAGCCGGATA	AGTGTGCAAA	GAAACCTTTC	TTGTTGCTGG	CGATTAAGTC	480
CCTCACTCCA	CATTTTGCCA	GAAGGCAAGC	AATCCGGGAA	TCCTGGGGCC	AAGAAAGCAA	540
CGCAGGGAAC	CTCGAG					556

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

GGAAACTTCT	AAACTATTTT	GCTCGCAACT	TTTACAACAT	GAGAATGTTA	GCCTTATTTG	60
TCGCATTTGC	TATCAATTTC	ATCTTGCTCT	TTTATAAGGT	CTCCACTTCT	TCTGTGGTTG	120
AAGGAAAGGA	GCTCCCCACG	AGAAGTTCAA	GTGAAAATGC	CAAAGTGACA	AGCCTGGACA	180
GCAGCTCCCA	TAGAATCATC	GCAGTTCACT	ATGTACTAGA	GGAGAGCAGC	GGCTACATGG	240
AGCCCACGTT	GCGTATCTTA	GCTATTCTGC	ACACGGTCAT	TTCTTTCTTC	TGCATCATTG	300
GATACTACTG	CTTGAAAGTC	CCATTGGTTA	TTTTTAAGCG	AGAAAAGGAA	GTGCTCGAG	359

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

GAGANACGAC	AATGTCCAGG	AAACAGAAAC	AGAAGGATTC	ATCAGGATTC	ATTTTGTATT	60
TGCAGTCCAA	TACCGTACTG	GCCCAGGGAG	GAGCTTTTGA	GAACATGAAA	GAGAAGATAA	120
ATGCGGTACG	TGCAATAGTT	CCTAATAAGA	GCAACAATGA	AATTATCCTG	GTTTTCGAGC	180
ACTTTGATAA	CTGTGTGGAC	AAAACAGTAC	AAGCATTTCAT	GGAAGGTAGT	GCCAGTGAAG	240
TACTCAAAGA	ATGGACAGTA	ACAGNCAAGA	AAAAGAACAA	AAAGAAGAAG	AAACTCGAG	299

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GAATTCGGCC	TTCATGGCCT	AGTAGCTGTT	CCAGTACAAT	TCAATGTTAT	CCAGGTTGGG	60
TGCATGTGTA	ATGATATTTT	TGTACTTTTG	TATCAACTCA	GAATTTCCAG	AGAGCTCTTC	120
CTGGCTGAAA	AGATGTCCAA	GGATCATCTC	CGGAATGGAA	GAGGTGAGGC	CTGTTAGCTT	180
GTGGGCTGCC	CAATCCATCC	AACCCTTGGC	ATTGGGATCA	ATGTTGATGA	GGACAAGACC	240
TTCAACAGTG	TCCGGGTGGT	TAAGAGCATA	TCTCGCCAGG	ATGTAGGCTC	CAGCTCCAAC	300

ACCAACTCCA ATTATTGTAG AGAAATTTAG GTACTGCAGG ACGCAAGGGA TCATGTCTGC 360
AAGCTGGTCC AGAGATGGGT ACTGATATCC CAAAGGGAAC ACAGGGGGCTC GAG 413

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

TTGGTATTGT CTCTGTACTA GTCTTTCCAA ATTCTGCTGT GAGCTTTTTG CTTAGACTGT 60
AAGCCTTAGA GTCATCATC ACAGTAATCC TAAAGACAGA TTTTCTGTCT CTATTGTGATA 120
AGGCCTTTTT GTGGGTTGTG CCGACTGTCA GTTTCATGTT TGTTTGTGTTG TTTTGGAAGT 180
GCAGTTACAT CCAGGAGACC TGTGGTGAGC ATAATGGGCT GTAGTTTGTG CAGTTGTCAG 240
TATAGCTTGT TAGGGAGCTC TTCCTGGGCA GAGTCTTGCA CAGCAGAGCC CAGTGCTGAG 300
CTGAGTTCTT GGCACCATCT CGAG 324

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

ACATTTCTTT GTAAGTNNN AAAAGCCTAT GAGGGTTTTT TCCACGATTC CGTCCCACT 60
TTGGCTTTTG TTGTTGTGTT GGCTGTCTT GGCCCCCTG GGCCCTGCAG TGGAGTGGGG 120
GGCTGCACCT GGGAGCCTCG AGCTGAGGCC CAGCCCCTCC TGCCCTGCAT TTTCTGCCA 180
AGCAGCACCT GAGACTCTGA AGCCGATGCC TATACAGGCA GAAACCTGCC AATCCAGCT 240
TGAACGACTG GAGGGTCTCG AGGATGGGGG TCCCTGGGGT GCCATCATGG GCAGGGTGCA 300
TCTGTTTGGG TATGCTGCCC CCCAGCTGGC GGGGCACCGG GGACAGCTCG AG 352

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GAATTCGGCC TTCATGGCCT AGGGAAAGGG AANGTGGGGA GGGTCCGAGG GGAAGGGGAC 60
CCCAGCTTCC CTGTGCCCGC TCACCCCACT CCACCACTCC CCGGTGCGCA GCCGAGTCT 120
CCTCTCTACC GCCACTGTCA CACCGTAGCC CANATGGATA NCACNGTTGT CAGACAAGAT 180
TCCTTCAGAT TCCGAGTTGC CTACCGGTTG TTTTCGTTGT TGTGTTGTTT GTNTTNTTT 240
TTNTTTNNN TNCGGAAGAC AGCAATAACC ACAGTACATA TTACTGTAGT TCTCNATAGT 300
TNCACATACA TTNATACCAT AACCTCGAG 329

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GAATTCGGCC	TTCATGGCCT	ATCCATTTCC	AAATCCACCA	AGGTCCAGTC	GACAGACATT	60
TCCAAAAAGA	ATCCTGTTCT	AGGACCACTT	GCGCTGAGAG	CACACCCGGG	GGTCAAAGGG	120
CAGCCACCGG	GGGTCAAAGG	GCAGCCATCA	GCTACTCCCC	AGGGAAGGGC	TTGGGGCCAC	180
CAGTCACTGC	AACCCCGCCT	CACCTCCGAT	GCCTGCTGTG	CCCAGGGTGG	TCCCGCTCAT	240
AGCGACGGCC	TGNGCGTNCA	TANGACCTCG	AG			272

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GATTGAATTC	AATGTTAAGC	ACCAATGCTG	GATTTGGTGG	TGGACTGAAC	ACCAAGTCTG	60
GCTTTGGTGG	TGGCCTAGGC	ACCAAGTCTG	GCTTCAGTGG	TGGCCTAAGC	ACAAGTTCTG	120
GCTTTGATGG	TGGGCTAGGT	ACCAGCGCTG	GCTTCGGTGG	AGGACCAGGC	ACCAGCACTG	180
GTTTTGGTGG	TGGACTGGGC	ACCAAGTCTG	GCTTCAGTGG	CGGACTGGGC	ACCAAGTCTG	240
GCTTTGGTGG	TGGACTGGTC	ACTAGTGATG	GCTTTGGTGG	TGGACTGGGC	ACCAATGCTA	300
GTTTCGGCAG	CACACTTGGC	ACCAAGTCTG	GCTTTAGTGG	TGGCCTCAGC	ACCAGCGATG	360
GCTTTGGCAG	TAGGCCTAAT	GCCAGCTTCG	ACAGAGGACT	GAGTACCATC	ATTGGCTTTG	420
GCAGTGGTTC	CAACACCAGC	ACTGGCTTTA	CTGGCGAACC	CAGCACCAGC	ACGGGCTTCA	480
GTAGTGGACC	CAGTTCTATT	GTTGGCTTCA	GCGGTGGACC	AAGCACTGGT	GTTGGCTTCT	540
GCAGTGGACC	AAGCACCAGT	GGCTTCAGCG	GCGGACCGCT	CGAG		584

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GAGAATGTCC	AGCAAGGAAG	TGAAGACTGC	TCTAAAAAGT	GCTAGAGATG	CAATCAGAAA	60
CAAAGAATAC	AAAGAAGCTT	TGAACACTG	TAAGACAGTG	TTAAAGCAAG	AGAAAAATAA	120
CTATAATGCC	TGGGTTTTTA	TTGGCGTTGC	TGCAGCTGAA	CTAGAACAAC	CTGATCAGGC	180
CCAGAGTGCC	TATAAAAAAG	CTGCTGAATT	AGAGCCAGAC	CAATTACTAG	CTTGGCAGGG	240
GTTAGCAAAC	TTGTATGAGA	AATATAATCA	CATAAATGCT	AAGGATGACT	TGCCTGGTGT	300
TTACCAAAAG	CTCCTGGATC	TTTATGAGAG	TGTTGACAA	GAGAAGTGGT	GTGATGCTCT	360

CAAGAACTT GTGGATCTAT ATTACCAAGA AAAGAAACAC CTAGAGGTGG CTCGAACATG 420
GCACAAGTTG ATAAAAACAC GGCAGGAACA AGGTGCAGAA AATGAAGAGC TTCATCTCGA 480
G 481

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GAATTCGGCC TTCATGGCCT AGGGGGAGTG GTGGGTATTG CTAAGTTATC AGTTATTTAA 60
CCTTATGGAG TTTTATTTAA CCGTTTTTGT TTGACATGTT TTATATATAT GTAATTTTAT 120
TTATTCTTCA CAAAATCCCT GTGAGGGGGG TGGTACTATT GTCCCATTT AAAGATGAGA 180
ACACTGAGGC ATGTCTAGAA TTCATCGAG 209

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GGCTCTGTGG AATTCCATGG CATCTTCCCC GCCCCCCCCA ACCCCCCCTT TCCCCCTTC 60
TTTTTTTTTT TTTCTTTTCT TTTCTCCCCT CCCCCCTTT CACCATTTC CCTCGGAGGC 120
GCTTCCCCG GGCAGGGGCA GAGCCGGTCT CACCCCCCGC CTCTCCCCG CCCCCCGCG 180
CCTATGGCGA GAGGGAGCCC CCTCCCAACC CGGGCTCGAG 220

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GAATTCGGCC TTCATGGCCT ACACATTCTT TTAGTCAGAA ACATTAAAAT AGTAGAGTAA 60
GTTGGCTTGA AGTGAATTT TGTGTGAAAT CTTTCTCTG CCTAGCCTA GTTTGTCCAT 120
GCACATTGTC ACACAGGAAG AACATTTTGA GACCTGCCAG AATATGCAAT GACAGGGTAA 180
AAAATGCCCG AGGTTGACTG TGTTCATAGA CATTGTGCTA AACACTCAAC ACTCCTGATC 240
ACACTGAATG CTTTGTACAG TCCTGTGAAT TGAGGGCTAT TATTATCCCC ATTTTATATA 300
TGAGCGAGCA GAGGCCCAGA CAGATTAACA AAGGTGCTCC CTCGAG 346

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

```

GCTTATACAG TGTCCGATAG ACACCAGGAA GCNACTAGCA GAGAATTGCG TACTCATAGG      60
TGGCACTTCT ATGTTGCCAG GATTCTCTCA CAGATTGCTT GCAGAAATAA GGTATTTGGT      120
AGAAAAACCA AAATATAAAA AAGCACTTGG CACTAAGACA TTTCGAATTC ATACTCCACC      180
TGCAAAAGCT AATTGTGTGG CCTGGTTGGG AGGGGCTATT TTTGGAGCAT TACAAGATAT      240
ACTTGGGAGC CGTTCTGTTT CAAAGGAATA TTATAATCAG ACGGGCCGTA TACCTGATTG      300
GTGTTCTCTC AATAACCCAC CTTTGGAAT  GATGTTTGAT GTCGGGGAAC TCGAG          355

```

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

```

GCTCGAGGGC GAAGGGGAGC AATGGCATTG GCGTTGGCCA TCCGTGACAC GGCATCCTAT      60
GCTCGCCAGA TGATGTTTAC GACCACCCCT CTCATTGTGT TCTTCACTGT CTGGATCATT      120
GGAGGAGGCA CGACACCCAT GTTGTCTATG CTTAATCATCA GAGTTGGCGT CGAGGAGCCC      180
TCGAAGAGG ACCAGAATGA ACACCACTGG CAGTACTTCA GAGTTGGTGT TGACCCCGAT      240
CAAGACCCAC CACCAACAA CGACAGACTC GAG          273

```

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

```

GAGATAAACA AAATTGATTG CCCATTCTC TCACTTCCCC ATCTTGCTT CCTAGACCCC      60
ACAGAGTTAA AACTTGGGAT TCCCCTGGCC CCCCAGAAC ACTTGATAT TGTGTTGTTG      120
AGGTTCTGTC CGCAGTAACA GACACAGTAT TTAATTGCAC ATACAGATGT TTGCTGGGTA      180
TATTCACTGT AAATTTTATT TAATCTGTTT TTTTGTTTGT TTGGGGGTTA TTTGGGGGGA      240
GGTTGGTTTT GTTTTAAAT ATAAAAAAA AAATCTGTCA CTCGAG          286

```

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

```
GGTCTGGAGG AGGCCCGGAG GGGCTGTGGG TGGACCACTG CAGTAATCTG GGTGAAAGAT    60
GATGATAGGC TAGACTAATA TGGTACCAGA GACAAAGAAG AGGGACTTGA GAGTTATTTA    120
GGAGGAAAAA AACAAAAACAA AACAAAAATC AACCCAGACTT ACGTTTTGAA ATAGGACAAG    180
TGAGGAAAAG GAGGGTTTCG AGAATAGCTT ATAGTTTTTCG AGAAGATGAG GTTGGACAAG    240
ATGCCACTGC TTTTCTTAGC ACTCTTCCTT CCCCTAAACC ATCCCGTAGT GCTCGAG      297
```

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

```
GAATTCGGCC TTCATGGCCT ACCCTCATTA CCCCAAGTGC CTCCTAATGG ATCTGTCCTT    60
ATTCTTCCTT GTTCTGTCTC CCTCATGCCC TGGAGCTCCT CTCTTTGGGA CCTTCCTCTC    120
CCAAGTCACC ACCCTCTCTC CCCTTCTACC ACTCAGCCAT TCCCCAGTTT CCACAGTTCC    180
TCAAAACATTA CCCCCTCCC CACTCCCAG TTTCTCCCC CTCCCCATTT GTCCCCCTCA    240
CCTGGGGGTC CCCGAAGTAG ATCTGCAG      268
```

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

```
GAATTCGGCC AAAGAGGCCT AGATGTGAGC TGGGGAAGGG AGGGTGGCCA GTAATGGGTT    60
TGTTATCAAG CAGGTTTGTT ATCACTGTGG GTGACAAGCC CCTTCCCATT TGGGGCCTCT    120
GGGATCCAGT GCAGAACATA TCCCTCGCAG GAGATGAGGA ACTGGGGTGT TCACAGAGTA    180
ATTCCTCCC TCACTAGTTG AGGGCTGCCT CTGGGGGTGG CTGAACTACC TCATGCAGCC    240
AGAGAAAGTC CTCAGGCAAT GAAATACAGA CACTGGCCAG CCAGCACTGA GGTGGCGAGA    300
CCTTACTGGC TGGTCCCCAG AGTGTCTGCA GCATTGTGTG AGATCTTAAA CTGGCTAGAA    360
GGACGGTAAC AGCAGCACCT GTTTCATAGG ACGTGAAGAT AGACGAGACA G      411
```

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:826:

```

GAATTCGGCC AAAGAGGCCT ACTAAAACCA TAATTGCTTG TTTTGGCTG TATCTGTCTT    60
TTCACGAACA TTTTGAGTTT AGCTCTGTCT TACATTCCCA TCCCTAAAGA TCATCAGGAC    120
TTTGTGTTTC GTGACAATGC TGGGACCAGA TTGGCCTTCA TCATCTCATA ACACCCTTAT    180
TTCCTATGGA AAAGTAAAT TGAATTATTC CAGATATGAT GACTTTAGGA TATCCTTTTC    240
CCTCTTGTA ATCCCTTCATT GTATTGTGT TTTCCCTTTG GTCTCCAACG TCCCCACCAC    300
CCCCAATCCC TCCACGACTT TTAAGCCCTT GGAAGCCAAC TTGATTAGTC AGG          353

```

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

```

GAATTCGGCC AAAGAGGCCT ACCGTGAGTT CCCAGGGTGG CCGGGAGGGG GAGCTGCGGG    60
GTTACAGCG GCTCCTCTCA ACGTTCCTGG CTCGCTCCC GACTTCTCAG CCCTGCCTGG    120
AGGGGCTCAG CCACTGCTTT TAGCTGTCTG CTGGCTTCC ACCCTCCAG CCTGAACCCT    180
GACTTCCCA TGAGGCCTTC CTGTGGCGGG GACACTCCAG GTCGCTGCAC CCCTTCTCTC    240
CTGAATTCT GTAACGACAT CTAACCTTTA TTTAATTAAT TTATTTATTT AGAGATGGAG    300
TTCTCTCTT GTTGCCCGG CTGGAGTGCA ATGGCACCAT CTTGGCTCAC TGCAACCTCC    360
GCCTCCAGG TTCAAGTGAT TCTCCTGCCT CGTCTCCTG AGTGGCTGGG ATTGCAGGCA    420
CCCATCTG                                     428

```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

```

GAATTCGGCC AAAGAGGCCT AAGCGGTATT TCAGCCACAG AGTTGGTGT GGGTTACTT    60
ATCTATTTG AATTTAAAG GCTTATAAAT AAAGCAGTGA CACTGCTTAC TGGGAAATGC    120
TGTACCAAAA AATGTTATCT TGCT          144

```

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GAATTCGGCC AAAGAGGCCT AGCGGACTAG GAGTCAATAA AGTGATTGGC TTAGTGGGCG 60
 AAATGTTATG CTTTGTGTT TGGATATATC TGGAG 95

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GAATTCGGCC AAAGAGGCCT AGTGGCTACC TAAATTGAGT ATCTGGCAAG AGTAAGATTA 60
 AGCAGTAATT TGTTCCAAAG AAGAATCTTC TACCAAGGAG CAACTTTAAA GAATGAAATT 120
 AACTTTCTTC TTGGGCCTGT TGGCTCTTAT TTCATGTTTC ACACCCAGTG AGAGTCAAAG 180
 ATTCTCCAGA AGACCATATC TACCTGGCCA GCTGCCACCA CCTCCACTCT ACAGGCCAAG 240
 ATGGGTTCCA CCAAGTCCCC CACCTCCCTA TGAACAAGA CTTAATTCAC CACTTTCTCT 300
 TCCCTTTGTC CCAGGGCGAG TTCCACCATC TTCTTTCTCT CGATTTAGCC AAGCAGTCAT 360
 TCTATCTCAA CTCTTTCCAT TGAATCTAT TAGACAACCT CGACTCTTTC CGGGTTATCC 420
 AAACCTACAT TTCCCACTAA GACCTTACTA TGTAGGACCT ATTAGGATAT TAAACCCCC 480
 ATTTCTCCT ATTCCTTTT TTCTTGCTAT TTACCTTCCT ATCTCTAACC CTGAGCCCCA 540
 AATAAACATC ACCACCGCAG ATACAACAAT CACCACAAAT CCCCCACCA CTGCAACAGC 600
 AACCACCAGC 610

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GAATTCGGCC AAAGAGGCCT AGGAAGAAAC AAGAACAAGA AAAAAGATTA TATTGATTTT 60
 AAAATCATGC AAAAAGTCA ACTCTGTGTT TATATTTACC TGTTATGCT GATTGTGCT 120
 GGTCCAGTGG ATCTAAATGA GAACAGTGAG CAAAAAGAAA ATGTGGAAAA AGAGGGGCTG 180
 TGTAATGCAT GTACTTGGAG ACAAACACT AAATCTTCAA GAATAGAAGC CATTAAGATA 240
 CAAATCCTCA GTAAACTTCG TCTGAAACA GCTCCTAACA TCAGCAAAGA TGTTATAAGA 300
 CAACTTTTAC CCAAAGCTCC TCCACTCCGG GAAGTGATTG ATCAGTATGA TGTCCAGAGG 360
 GATGACAGCA GCGATGGCTC TTTGGAAGAT GACGATTATC ACGCTACAAC GGAAACAATC 420
 ATTACCATGC CTACAGAGTC TGATTTTCTA ATGCAAGTGG ATGGAAGACC CAAATGTTGC 480
 TTCTTTAAAT TTAGCTCTAA AATACAATAC AATAAAGTAG TAAAGGCCCA ACTATGGATA 540
 TATTTGAGAC CCGCCGAGCT CGAG 564

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GAATTCGGCC AAAGAGGCCT ANTCTGTTGA GATTTCCTCC TTAGTTTCC AACCTTCTCC	60
CCACCTACTC ATTTATCCAT CCCTCCCACC AACTCATTTA TCCATCCCAC CCACTCATTT	120
ATCCATCCAT CCCACCCACT CATTTATCTG TCCATCCCAT CCACTCATTT ATCCATCTAT	180
CCCACCCACT CATTTATCTG TCCAACCCAT CCACTCACCC ACCTACTCAT TTATCCATCC	240
CATTCGCTTA CCCATCCATC TATCCCACCT AACAATACAT CCAACCATTG CCTCACCTAT	300
GCATCTGTCT GTTCAGCTGT TCATCCATTG ATTGATCTTT CCATCCATTG ATCCACTCAT	360
TCACACACCT ACCTACCTAC CCACCCGCTC ATTTATTAC CCACCTACCC TCTCATCCAT	420
CCAG	424

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GAATTCGCCA AAGAGGNCTA GTCTACATCA GCTAACTTTC CTACAAGATT ATCAAATTTT	60
ACACAGTATT TTTCTGTATT TAATGACTGC CATGGTCTGC AAAATTATGT GATTAGACAA	120
TGAATGACGC TTAAGAATG ATGACCTATT TTCTAAAGTA CACTCAAAT ATTAAGTTT	180
AGAGACAAAG CAAAATCTAT CATAAAGTTG GCTTCTGTTG ATAGAAACAG AGAGGTAGGT	240
TAATAATCAC TGTCTAAGA TAAGCNAGAA TGCTTAGAAA TAAAAGTTGA GACCTGCTT	300
CAAAAAGAG AAGTTGAACC TTCCAGCCCT GAGTTTCTAA TATTACATGA AAATTATGAA	360
AATGAGCATT AAGCCAGTCG CAG	383

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GAATTCGGCC AAAGAGGCCT ACTACGTAGT TGGAGCTNTT TCTTCCCCCA GCAAAGCCAG	60
AGAGCTTTGT CCCCGGCCTC CTGGACACAT AGGCCATTAT CCTGTATTCC TTTGGCTTGG	120
CATCTTTTAG CTCAGGAAGG TAGAAGAGAT CTGTGCCCAT GGGTCTCCTT GCTTCAATCC	180
CTTCTGTTT CAGTGACATA TGTATTGTTT ATCTGGGTTA GGGATGGGGG ACAGATAATA	240
GAACGAGCAA AGTAACCTAT ACAGGCCAGC ATGGAACAGC ATCTCCCCTG GGCTTGCTCC	300
TGGCTTGTA CGCTATAAGA CAGAGCAGC CACATGTGGC CATCTGCTCC CCATTCTTGA	360
AAGCTGCTGG GGCCTCCTTG CAGGCTTCTG GATCTCTGGT CAGAGTGAAC TCTTGCTTCC	420
TGTATTCAGG CAGCTCAGAG CAGAAAGTAA GGGGCTTACT CGAG	464

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCGGCC	AAAGAGGCCT	ACTGGGAGTT	CGGAGTGATT	GTTTCCTGTT	ACAGGCCAAA	60
AAATTTGTTT	GGTTACTTAG	TGGTAGCATT	TTGAGAGGAA	AGTTTACAGA	AAACTAGGGT	120
TATTTTGTGA	TTATGCTTGA	ATTGTCTTTA	TTGTTTCCAA	GGCATCTTTT	TTTTTTCCTT	180
CTAGTTATCA	AGATGTTAGG	TTCTGTGCCC	TTGTGGGCCT	TCCCTCTGCC	CAAAAAAAGC	240
ATGGATGAGC	AGAGTAATAT	CATTAAATG	GCAGTCTTTG	TTAGTTTTC	TAGAAAAGAT	300
GGTCTCGAG						309

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAATTCGGCC	AAAGAGGCCT	AAGGCAGGTT	TTTTTTTCTA	TGCTTATTGA	TTAGCCTAT	60
CTATTTATAA	CAGTATAATT	CAGAATATAA	ATATGGAACA	AGTTTCATAA	GGAAGTTTAT	120
CTTTAACTCA	GACATTATAT	CATTAATACT	TCAAATCTCA	TTATACCATT	ATGACCTGAA	180
TGCTACATTT	TTCTTCTGT	ATGGAGAGCT	TAGGGAAAAA	TTGTGGCCTG	ATGTCTTCAT	240
CCATTCACTT	ATCATAGAGT	ACATAATGAT	CTCAAATATC	CAAAAATGGT	TATATTCAGC	300
TGCATATTTC	TAAGAAAAACA	GGCAGGACTC	GAG			333

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GAATTCGGCC	AAAGAGGCCT	AATTGATTTC	CCATGAGTCT	TGTAATCTTT	GCTCTGCTGA	60
TTGCGTTTGC	CGTCTCTAGA	CCATCTCGCT	TCGAACAAAT	CGCAAAAGAG	GTGAATTCCA	120
GAAGAACGAC	CTGGATTGCA	GAAGAATCGG	CTCCGTTCCG	TGACTATGCT	CGTTTGATCG	180
GTACCCCTTC	AAATACGGTC	CCTCTTCCGA	GTAAGACTGT	CGATGTCGTG	AAGAACCCTC	240
CTGAGAGTTT	TAACGCATTG	GAAAAGTGGC	CGGAATGCAA	GTCCATCACG	GAAATCCGTG	300
ATCAAGGAGA	ATGTGCTTCA	TGTTGGGCAC	TGGGGAGTGG	CGGAGGTGGC	CACGGATCGT	360
CTTTGCATTT	CTTCCAACGG	AAAGGATCAA	TCCCGTCTCT	CTGCCGAGGA	TCTGTTGGGA	420
TGCTGTGACT	CTTGTGGAAT	GAAATGCAAG	GGAGGGTACA	CGGGGAATGG	CCTGGGAGTA	480
TGTACGTCAG	GTGGGAATTG	TGACGGGTGG	AGCGAATGGA	AACAAGGAAT	GGTGTAATGA	540
GTACGCGTTC	CCGAAGTGCA	GTACGGGTAT	TCAGGGCTCC	TATCCTGAAT	GCTCTTCCAT	600
CCCCCCTGAA	GATCCGGAGT	GTTCAACGAC	TTGCATAAAG	GGGTATCCCA	TCCCATATGA	660
TCAGGACCGT	CACAAAATGA	AGTCAGCCTT	CCAGCTGGCA	CTCGAG		706

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GAATTCGGCC	AAAGAGGCCT	ATAAAAGTCT	TATTTTTTAC	TTTGTCCTACT	GGAATACATC	60
ATCGTTGGCC	TATCATTCCA	AACTCCCTAC	AGTGTTGGCTT	CAGCTTATCT	CTCTCTGTTT	120
TTTACAGGAA	TCCTAAACTC	TAACCCAGGG	ACCTCAACA	TCTGTGCTGG	GTGGACTGTG	180
GCCACATTTT	CAGCTGGCCA	GTGTAAGGGT	TTTAGAGGCC	CTTACATGAG	AAGAAATACA	240
ATTTTAAAGT	CTCTGAGATG	ATGTGCTTCT	TACATTTTGT	GAATTAAAT	GCCTCTTTAC	300
TTATAAAATG	CTGGTAGTAA	TAGATGGTCA	TTATCTCACT	GTCATTTGTG	AAAGAAAAAA	360
CGATTGTAAT	AGAATCTTGT	CTATTTTTTT	TCTCTAAGGG	AGGTAAGTTT	TCTCCCTAAG	420
CAAACCTTAT	GGAATGCACA	ATGCTTGGCT	TTACCTTCT	TTTATTCTCA	CTACCACCGG	480

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GAATTCGGCC	AAAGAGGCCT	AGAATTAAGG	TGTATTATGA	GCAGTTGAAG	ATATATAGGA	60
AATTTTTTCC	CAAACCACTA	TCTCTGCTCG	TTCTATTTCAT	TCAGTCTGTT	TATGTTATTC	120
CTTCATTCAT	TCATTTTATA	GAACAGTGGA	GTGCCTACTG	TATGCATCTA	TTGTTCTGGG	180
TCCTGGGGAA	AGAAAACAAA	GTTCTGCTT	TCATGGAACT	TACATTATAT	TGGCGGAGAC	240
AGTAACAGAC	AAACAAATGT	AGCCTGTGTA	CATGTGTTAC	ATGAAAAGCA	GGGTAGGGGG	300
CTGGGAGAGA	GTAGTAGGGA	GTGCTATTTT	CGAGGTGGTT	GTCAGGAAAG	GCCTCACTGA	360
GGAGGTGGCA	TTTGTAGTAG	ACCTGAGCGC	AGCGGGGGCG	TAAGCCCAGG	CAGCATGTGG	420
AGGAAGAGTG	TTCTTGGTGA	AAGGAACAAG	GATAGAGGCC	CGAAGCTAGA	GAGCTCAGCA	480
TGATCAAGGA	ACAGCAAGCC	CCGTGTGGCT	GGAATGGAGT	GAGCAAAGGA	ATGAGCAGTA	540
GAAGGTGAGT	GAGTTGGGAG	GTCACCAGAG	ACCATGGCAA	AGACTCGAG		589

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GAATTCGGCC	AAAGAGGCCT	AGGGACTAAC	TGCAACGGAG	AGACTCAAGA	TGATTCCTT	60
TTTACCCATG	TTTTCTCTAC	TATTGCTGCT	TATTGTTAAC	CCTATAAAGC	CCAACAATCA	120
TTATGACAAG	ATCTTGGCTC	ATAGTCGTAT	CAGGGGTCGG	GACCAAGGCC	CAAATGCTCG	180
TGCCCTTCAA	CAGATTTTGG	GCACCAAAAA	GAAATACTTC	AGCACTTGTA	AGAAGTGGTA	240
TAAAAAGTCC	ATCTGTGGAC	AGAAAACGAC	TGTGTTATAT	GAATGTTGCC	CTGGTTATAT	300
GAGAATGGAA	GGAATGAAAG	GCTGCCCAGC	AGTTTGGCCC	ATTGACCATG	TTTATGGCAC	360
TCTGGGCATC	GTGGGAGCCA	CCACAACGCA	GCGCTATTCT	GACGCCTCAA	AACTGAGGGA	420

GGAGATCGAG

430

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GAATTTTAC TTGTCTATAG TCTAGTATG TTATACCATG TGGTCTTGT ATAATCATGG 60
 TTTCCATTCT GTGAGTCTTC AGATTATAGG CCTCTTTGGC G 101

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GAATTCGGCC AAAGAGGCCT AAATGGCGTC GTGGCATTGA GGGGCATCCC TCCTAGAACC 60
 TCCAGGAAAA GCTCGCGGAA GACGAGGTTG TCGGGAGAGA GAGGCTCCAA GCAGTCTGGG 120
 AAGTGTAGTC CAGTTGGCTT AGCAGTAGTT TCGTTGGGGG GGAGCCGAGG TTCCGGGAAG 180
 GGGCTAGGCC GGCTTGAAAA GAGATTATGA CTGTACCTTT TAACTTTGTA GCTGGAACAC 240
 AAGAAGTGTT TGTTTAATGA ATGACGTACA CATTAAAGAT CTGTTTGGAC GCGGAGGATA 300
 ATCCTGTGAA TTGCTAATAG TTCACTGGGT TTGGCCCTTA GTGTTGACTT CAGTATGCTG 360
 AGACGGAAAC CAACACGCCT AGAGCTAAAG CTTGATGACA TTGAAGAGTT TGAGAACATT 420
 CGAAAGGACC TGGAGACCCG TAAGAAACAG AAGGAAGATG TGAAGTTGT AGGAGGCAG 479

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

TGGAAGAGCT AACTCGTCTG GCCTTIGAGC TCTTTGCTGA AGAGCAAGCA GAGGGTCCCA 60
 ACCGCCTGCT GTACAAAGAC GGCTTCAGCA CCATCCTGCA CCGCTGCTG GGTTCACCCC 120
 ACCCTGCTGC CACAGCTTTG CATGCTGAGC TGTGCCAGGC AGGATCCAGC CAAGGCCTCT 180
 CCCTCTGTCA GTTCCAGAAC TTCTCCCTCC ATGACCCACT CTATGGGAAA CTCTTCAGCA 240
 CCTACCTGCG CCCCCACAC GCATCTCGAG 270

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

```
GAATTCGGCC TTCATGGCCT ACACAGCCAG TATCAGAACC TCAAGAAAAC GAGGACACTG      60
GGGACAGGGA CCAAAATTCA GACCACTTTT TTCTCTTGCC TTCAATAGG ATATTCTGTT      120
AATTGAATTC ATCTGAAAAT CAAGGTCATT GCAGAGAAGT CAGCATTCTA GAGCACAGAA      180
CAGGGCAAAA CAGGACGAAA GATGGATTTG GAGACCAAAT GGAGAAGGAA GAACAGAGAT      240
ACGTGTGCTC CAAATATGAC ACCCAACTTC TTTACTCAGA GCAGTTACAT GTCAGATTAT      300
ATTTTAGTTT TTCATTTCTC CTATAGGCAT ACATACTACA AGTCTATAAT AGAAAAGTAG      360
TGGCTGGGCG CGGTGGCTCA CGCCTTTAAT CCCAGCACTT TATGGCGCTC GAG          413
```

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

```
GAATTCGGCC TTCATGGCCT AGGCTCTGTC TACCAAAAAA AAAAAAAAAA GAAAGAAATC      60
TTGCAGTCTG AATACATGGT TGTGTTCTTA AGAAACCTGG TGATAACAAC GACAAAAGTC      120
CTCGAG                                     126
```

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

```
GCTTCATGGC CTAGTTGAAT AGTCAGTTAG AAATGGAAAG AATGAAAGTT GAACAAGAAA      60
GACAAAGCCT TAGAACAAAA GACACAGCCC TAGAACAGAA GGACAAGGCC CTGGAACCAA      120
AAGACAAAGA CTTAGAAGAA AAAGACAAGG CCCTGGAACA GAAGGATAAG ATTCCAGAAG      180
AGAAAGACAA AGCTTTAGAA CAAAAGGGCA GAGACTTAGA GCAAAAAGAC ACAGCCCTAG      240
AACAGAAGGA CAAGGCCCTA GAACTCGAG                                     269
```

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

```

GCGATTGAAT TCTAGACCCA CCTTCAGACC ATCTCGGAAG ATCTAAAAAG CCTGACCATG      60
GACCCTCACA AACTGCCCTC CTCAAGTGAA CAGGTGATTC TGGACTTGAA AGGTTCTGAT      120
TACAGCTGGT CGTATCAGAC GCCACCCTCT TCCCCCAGCA CCACCATGTC CAGAAAGTCC      180
AGTGTCTGCA GCAGCCTGAA CAGTGTCAAC AGCAGTGACT CCCGGTCCAG CGGCTCCCAC      240
TCGCATTCCC CCAGCATTCT CGAG                                         264

```

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

```

GAATTCGGCC TTCATGGCCT AGAACATTCC AAATTTTCTT GGTTC AATA CCCTTTTTTT      60
TCCTTTGAGG GGAAAAGAGG GGAGAAAAC AGGAGTGATG TCATTTCTTT TTCATGTATT      120
CCAATTAAAG AAACAAGGCG AGGTCGTATA ATGGCATATT AATACATTAG ACTTAATCTA      180
GAACCCCTGT AGCTTTTGA TGTGTTTAT TTCTTATCTC TTGAATTCC TGTTTGGTTA      240
CTTGCTTCC AATGGAGGTG AACTTAACAA CCATACTGA ATATTCCGTC TTGACTTTGT      300
AAACTGTGGC TACTTGAAAT GAAGTTTATC TGGGGTCTCG AG                               342

```

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

```

GAATTCGCCT TCATGGCCTA GGTATTCTA TTATTGTAG CTGAAATAAT TCCTGGCACA      60
AATGACTTTG AAATTTATCT CTGAACATCC CAAATTCATT ATTAGCAAAT ATCAGAAACT      120
TCACATCACT CCAGTCTGTT ATTTACATG GTTTTCTTAG GGCTGGAAA GTTTTACAG      180
CTGGCTTTTA TTGACTGTGG TGGCTGATAT GCTGAAGAAT GGAGCTCATT GGTGTGAGGC      240
TTCTGCCAG                                         249

```

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

```

GAATTCGGCC TTCATGGCCT AGACATGAAT TCTTTGACTT GTGCTCATTG TTTCTGAACT      60
TATTGAGGCT TATATATATC AAATAAGGTT AATTTACACA ATAATTATTT TTAATAATTA      120
ATAAACTCAT TCATGTAGTA TATTTTAAAA CATTATTTCC TCTCATTTTT CCTTCTCTTT      180
TTTCTTCCTA TATATTTTAA AGGTTTCAAG AGAAAACGGG CTTTCAGTTT TAAAAAAATG      240
TAGACTTGCA TTTTACTGT GCTTATTTAA AATAATGGAT ATAATTTATA TTAAGGTCCA      300
AATTATTTTA TTCACAGGAT AATCATGGTC TCTGATAAAA GATGCCACA TTTCTGTGTA      360
CTCACAGTTG TTGTATATTT TCAATTTCA ATTTTGAAAG TAAACTCAAC ACTCGAG      417

```

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

```

GAATTCGGCC TTCATGGCCT AGCTAGCTAT TGTAATAACA AATAATAAAG TCTGCATTTC      60
CTGTCTTCTT TAAGCCTTCA TTGCCTATTA AATCATTACA TTTTAGATTA GATATTATAT      120
TTTGATCATT TGAGGAACCA AATTAAAAAT ATGGAATAAG TATGGCATTG AATTATACAT      180
GCCTATTGCT AATATATTCA TATTTTATAG GATTTAATGA AACAGTCTCC CAGCTCGAG      239

```

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

```

GAATTCGGCC TTCCCTAGGA AAGTTCTTCA CATCAGGAAA CATTAGATCA TATACAGAAA      60
CAAATAAAT TTGATAAAGT AGTTATGGAG TTTTGCATG AGTGTATGGT GAATAAATTC      120
AAGAAAACAT CTATTCGTAA GCAACAGACA AATAATCAAA CAGAAGTAGT TAAATAAATT      180
GAAAAAGATG TTATGGAAGG TGTTACTGTA GATGATCACA TGATGAAGGT AGAGACAGTT      240
CATTGCAGCG CTTGCAGTGT GTATATCCCT GCTTTACATA GTTCAGTTCA GCAGCACTTA      300
AAATCTCCTG ATCATATCAA AGGGAAGCAG GCTTATAAGG AACAAATAAA AAGAGAGAGT      360
GTCTTGACTG CTACAAGCAT TTTAAATAAT CCAATAGTGA AGGCGCGATA TGAACGTTTT      420
GTAAAGGGTG AGAATCCTTT TGAAATTCAA GACCATTCTC AGGATCAGCA AATAAAAGGC      480
AGACTCGAG                                         489

```

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

```

GAATTCGGCC TTCATGGCCT ACTTCACTAA CCTTTTGT TTTAAATGA ACCTGCTACT      60
TAAAAAAAT ACACATCACA CCATTATAA AGTGATCTTG AGAACCTTT CAAACCAGAT      120
GGAGCATTGC TTGCAAAATT TTTTCTCTA TGTTTGCATG CGCTCGTGTG TGTGTGTCCA      180
GGCAAGAACA CATTTTATAA AAATAAGAAC ACTTGGGCTG GGCATGGTGG CTCATGCCTG      240
TGATCGCAGC TCTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

```

GAATTCGGCC TTCATGGCCT ACACAGCTGC AGTCAACATC CACAACTACC GGGACCACAG      60
CCCCTACTGC TGGCTGGTGT GGGCTCCAAG CCTTGGCGCC TTCTACATCC CTGTGGCTTT      120
GATTCTGCTC ATCACCCTGA TCTATTTCCT GTCGCCGGGC TACGCTTACG GGGTCCTCTG      180
GCACAGAACC CCAAGGCGGG CAACAGCAGG GTCGAG

```

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

```

GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAAAATAAA TAAATAACCC ACAGAGCTGA      60
GCACAGGCTT CTTATGCTT TTCTTTGGA AGGTGTCCTA GATATATGAT GATTTCTTTT      120
TTCTTTCACC TCCTCTTGAT TGTCAAGT AGCTTGCTTG GCTCAGGAAC AACAGAAGAG      180
AATAAGAAA ATGACCTCAG ACCTTCCTTA CCTCAGTCTT ATGCAGCGAC CGCAGCCAGA      240
CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

```

GAATTCGGCC TTCATGGCCT ACTGTCTCAA AAAACAAACA AACAAAAAGA AAGAAAGAAA      60
AAGGAAAGGT AGACTTATAT AAAATAGACA GTAAAGCATA GGGCAGCAGA AAGGAAACC      120
TACTCGCAA AAGTCACTTG TTTAACCTC ATCCAGGAGC TTCTCTAAG TTCACCTTTA      180
TTTTTCACAC GTCCTGGGTC CAAATCCCAC CATGCTCTGC CGTATTCTTG CCCTTTGCTC      240
TGTTGTTGAA AGAGTCATGA GCGAGGCCTC TCTATGGATG GTTCCAATGA GCCACATGAA      300
CAAAGCCATC GTCAGTAAGC AGCCACTTCT CGAG

```

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GAATTC	CACT	TGATCA	ACTT	AATTC	CTTTT	CTTTAT	CTTC	CCTCC	CTCAC	TTC	CTTTTC	60
TCCCAC	CCTC	TTTCCA	AGC	TGTTTC	GCCTT	TGCAAT	ATAT	TACTGG	TAA	GAGTT	GCAGG	120
ATCCTC	GAG											129

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GAATTC	CAAGC	ACCATA	ATTT	GGCCACT	CAG	CTGTCAT	CAG	GAAC	TAGCC	AACATTC	CTT	60
TTCAG	AAAAA	GACTTT	GGAG	AGGGG	CAAAC	ACTTCT	GACA	GTCAT	ACTGT	GTA	CTTATTT	120
TAGAAA	ATAA	GCTGCT	CTCA	GGCTTC	AGTA	TCCAGT	CAAA	TATAAT	ATAG	AAC	CTAGTC	180
TGTTTT	GAGT	CCTACT	ACAA	TAATAT	TTTC	ACAATAG	ACT	ACCAGT	TATG	AAGTT	CTCAC	240
ATTTT	CCCG	CATGCT	CGAG									260

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GAATTC	CTGT	CCCAC	TGCT	GAATG	AGTGC	GTGCC	AGCTG	AACAT	CAGCG	TGGCT	TCGTT	60
CTTCA	ACACA	TTTAC	AAAAG	AAGTA	AAAAAT	AAACAG	TTTT	TTCTT	CTCAA	TTCTC	CTCCC	120
TGCTT	TTTTTC	CTTTG	GAACC	ACAAT	CATGC	CCAGT	AAGT	GCTTT	CCTAG	GTGAG	AGGTG	180
TGTGT	CCCCAG	GTTGA	AGGCA	AGGCC	AGTGG	TCTCG	AG					217

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

```
GAATTCGGCC TTCATGGCCT AGAATATTTT TATCATCCCA AAGCTAAAAC ATTAAAAAAT    60
TTAAAGTTTA TTCTTAGAGA TTGATGCAAC TTGCATATCT AATCGAG                      107
```

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

```
GAATTCTAGA CCTGCCTCGA GGGCATCCTT TACTTTTTTT TTTAATTCAG CACAAACCAA    60
ACAAAATTTT AAAATTTGAT GAGATTTGAA GTTGGACAAA AGTGTTATGC AGTTTTAAAA    120
ATTTTTTTTT TTTTTTTTGA GACCAGATCT CACTCTGTG CCCAGGCTAG AGTGCAGTGG    180
CATGATCTCA GCCCAAACCT CTACCTCTTA GGCTCAAGCG ATCCTCCCAT TTCAGCCTCC    240
CAGGTAGCTG GGAGGCTGAA ATGGGAGGAT CAACTCGAG                      279
```

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

```
TGTATTTTTA CGTGACCTGT TTTCCAGAAT TTATGATATT TCTATGGTTG GTATTCTCAA    60
TTTTGCAAT GTGTCTGGT GTGGAACCTT TTCATTTGTT TTGCTGGGGA ATTGATGGAT    120
CCTTTGCATC AAGATGCTTA TATTATTCTC TCAGTTCTGG GAAACTTCCC TGTATTATTT    180
GTTTGATAAT TGCTTTCTCT CTGCTTTCTC TTTTCCGTTT TTTGGAATTG CTGTGTTTGTG    240
TGTTGCATTA CTGCAGAGAA CTCGAG                      266
```

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

```
GAATTCGGCC TTCATGGCCT AGTGCTGTGG TAGTTTGTGC CTTTAGAGGG ATTTGTGTAT    60
CTCATATAAT TTAATTTTTT GACATTCAC TTTTCACAAT ATTCTGTTAG AATTCTTTTA    120
ATTTCTGTAA GGTGATATCT ATACTTTCAT TTATGTCTAG TAACTTGAAT CTTCTCTCTT    180
```

TTGTTCTTTC TCGGTCAAAC TAATAATACG TCAATTTTAC TGATATATCA GAAGAACCAA	240
CTTTCAAGTT TATTAATTTT CTCTATTGTT TTTATTTTCA CTACTTATCT CCATGCTAAT	300
CTTTATTATT TCTTCCTTCT GTTACTTTG GSTTAAGTCT GCTCTTTCAC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GAATTCGGCC TTCATGGCCT AGCTTACTTT ACAATTCTGC TGTGTGCAA GTGTTCTAT	60
AGTTTTTTTT AAAGGTATGT TAACTATTTT TCCCTTTTGG TTTATATTTG TAGGAATCTT	120
TGCCCTTAAG TGTGCCCCGTG CAGAAGAATT ATTTAACATG TTGCAAGAGA TTATGCAAAA	180
TAATAGTATA AATGTGGAGC TCGAG	205

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GAATTCGGCC TTCATGGCCT AGTCACTTGT TCTGTAGAAT ATGTTCAAAT CTGATTTTGT	60
CTTTTGTGTT TCTTGTGTTA TTACCTTGTT CCTCTATCCC CTGTTTTTTC TGAAAATGAA	120
AGTTAGCTTA GAAGTTTCAT TCCATTCTGG TTCAAAATGC TTAAGTGCTT TATGTCGTGT	180
CATATTAGGA AACACAGTAT CTAGTGGTCC CAATTTTAGT GATTCAAAAA TCAGTCTCTA	240
GGTTCAGAGA TTAATCAGTA GATTCAGAGA TCTCTCCATT GTAAATTCT TAATTACCT	300
TTGAATTGCT AATGTTCTGT TCACTGATCG TTGTGGCCCA AATTATTTAT TTCCTAGGG	360
GACTCGAG	368

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GAATTCGGCC TTCATGGCCT AAGGAGCAGC AGGAACATGG TACATAAAAT CATCTGCTT	60
CTTATAATGG CAGGAATCAG TGGGATATGG TATTTGTGCA GCATGCTGGG GCATCCACTA	120
GAAAGGCCTG AAGGAAGACT CGAG	144

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

```

GAATTCGGCC TTCATGCGAT TGAATTCTAG ACCTGCCTTG AGCCCCTCCA CCCCCAAATC      60
CTTCCTCTCC TCCCAGTCCC ACCCCTTGCC CCACGGAGTC CTGGGGACGC AGTGCCCCAG      120
CTGGGAAGAG GCGGGGATCG GGCACCTGGT CCTCCTTGTC CCCGCTTTCT TGGGGGCTTG      180
CTACTTTTGG TCTTCTATTG TGTGGCTTTC TGAGTATTTC AACCCACAGTC CTGTGTCACC      240
TTCCTTTTTC CTTCGCTGTC CCCTCGAG                                         268

```

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

```

GAATTCGGCC TTCATGGCCT ACAGAACTAT AATTTATCTT AGTTTAAGCC ACTGGTAAGT      60
GTAATTGTAA TTGTAATTG TTACATCTGC TATAGTGAAA CTAATACTGA AATTAGAAA      120
AGATGGGTAA CTTATTATGT GGTGAAGTTT AAAAAAGATA AGTAACTCGT TGAAGATCAC      180
ATAATTAGAA AAGAAAGCAG TAGAGCTTGG CCTTGAAGTC AACCAGTGTG ACTCCAGAGC      240
TTGTAGAACA GAATAACCAC CTCCAAGGCC AGCTGAATCT GACCACAGTC TGGTGGAATT      300
CTAGTACATC TCGTTGAGAA GTGGGATTGC CGGAGGGGAG TTGGTTATTG ATGAAGGTGA      360
TGATGTTTGT CCAATGTCCT CGAG                                              384

```

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

```

GAATTCGGCC TCATGGCCTA CTTGGAGAGT TTTGTAAGGA GAGTGGCAA CATAGCACGG      60
ACTAATGCCA CGAACAACAT GAATCTAAGC CGAAGCAGCA GTGATAACAA CACTAATACT      120
TTGGGGAGGA ATGTGATGAG CACAGCAACT TCTCCTCTTA TGGGTGCTCA GAGTTTCCCT      180
AATTGACCA CACCTGGTAC TACATCAACA GTGACTATGT CAACATCCAG TGTACTAGC      240
AGCAGCAATG TAGCTACAGC AACAACTC GAG                                         273

```

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

```
GAATTCGGCC TTCATGGCCT AGGTCAGGAG CTTCTTGA GTCCCAATTC TGCATCCCCA    60
AATGATAAAG ATGGGGTGAA GGAAGTGA GAAGTGAAGT GGAGAGTCCT CTTGCTTGAG    120
GTCCCTGAGA ATGTGGTCCC GGAGTATCCG GATCACTGGA AGCCAGGACT TCAACGCATT    180
GGGTAGTGAG GGATGGAGGG AGGGGCTGGA CGCAGAAGCA GGATGAAGTC TGCTGGGTGT    240
GAGCCTCCAA GGAGGTAGAA CAAAGAGGGC AACTCGAG    278
```

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

```
GAATTCGGCC TTCATGGCCT ACCAGACTCC CATAATAATA AACCTGGTA ATAAACAAAG    60
GAAGTCTTTC CAGTTTCAGT GTATCAACCA CCACGTACCA GATAAAATCT TATTTACCT    120
TTCACAATTT ACCAGTGTG GGCTGTGAAT TAATATTTT ATTTTCTGT GCATTCATAA    180
ATTAAGATTA TTTTATTGTA TTGTAAGTGT AATTTTGAGA CTAAAGTCTA AAAACAAGAC    240
ATCATGAAAT GGAGCTGGAG GATACTCGAG    270
```

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

```
GGTTTAGAAA GGGCACAAAC AGTGCAAACC TGTTTCATGAA CCTTTACATG TCATGAACAG    60
GGCAGAATGC TTCAGGAAAG AATTGTCGAA AGTAAAAAAG CAAATAATGG ATGCAGCTTA    120
TTCTAGTTAT TGAAGAATCC AACGGGATGG AAGCTAAATG TAGCACATGG CATGGGCGAT    180
GTCTCAACAG TGAGTGGGAT AACAGTCGT TTTAATGGTT CAGGGCCAAT AACCGGGGAG    240
GGTGAGGAAC GGCATCTCTG TTTTGAGTAA ACAAGAGTGA TTTCCCTTCC TGACACTGAA    300
AAATGAAACC TTTGGGAGAG TAGAGGAAGC GATCTCGAG    339
```

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCGGCC TTCATGGCCT AACCTTTAAA CCCTAAAATC CAGGAAAAGA AAATAAATAC	60
ATTATCATGG ACCTGAGGGA TTTTACCTG TTGGCTGCTC TGATTGCCTG TTAAAGGCTG	120
GATTCCGCAA TAGCTCAAGA ACTTATTTAC ACTATTAGAG AGGAATTGCC TGAATATGTG	180
CCCATAGGAA ACATACCAA GGATCTGAAC ATTTCTCACA TCAATGCTGC CACAGGGCCA	240
CCTCG	245

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

GAATTCGGCC TTCATGGCCT AGTTTCTTC ACTGGCATTG ACAAATTTAA GCCATTGCTG	60
CCTCATTAGC CTTGTATTTT GTGTGCATAT CATATATCCA GACCTGTATG TTCACTTTAA	120
GCATTCTTAT ATCACACTGT CTCCTCATCT ACCATATGGT AAATGTTAAA ACTCCACATT	180
TGTCTGCATC AGGGAATG CATGGGCACA CATCCTCCCC CCCTTCCCTC GAG	233

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

GGACAGGAAG TCAACTTCAA GCAGATTGAC TTGAAACGGG ATCTCATTTA GGAAGCATAA	60
GTGTCCAATC AAAAAGTGTG TATTTTTTTA AATTGGAAA ATACTCAAGT TCCAGTTGCT	120
TATCATTTCT CTTCACTTTC TGAAACCTG GCAATCCCAT GTGGACTTCT GGTAGAATGA	180
GCAATGCAAA GAACTGGCTT GGAATTGGCA TGTCTTGTA CTTCTGGGGG CTGATGGACC	240
TTACGACCAC CGTTCTCTCG GACACCCAC ACCTCGAG	278

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GAATTCGGCC TTCATGGCCT AGTCCTCAA TTAGTTATTG CATTATTTTC AAGTATTGTA	60
TTATCATTTA TTGATATTGG TAGTGTTC TAAAACAGGA AATACATAAT TTGGCATCCT	120
TATCTTAGT TTTATACCTA AAGAACTAG TAACTCACAG GAGAACGTAG TAACATTATC	180

ACTTGTTAAT CAAGCTTTCA GTGAAACAGT TTATCAAACC ATTTTTTTTA TTTTGATTCA 240
GCAAATTTGT CAACTAAATT TAATTTAAAA GTAGAGGTCC AAAGCTCGAG 290

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

GAATTCGGCC TTCATGGCCT ACTCAAATTG GAAAGAAAGA TTCCTTGAGA CTTACTTTTA 60
AAATCTAAAG TGTGAGGNNNA ACANCAGAGT AAAGNCCAGA CTCATTNNAC CTTTCGATGTC 120
TGCATAGATC CAGNAGTTGT ACATTTTACC TAACAACATC ACTTTTGTG AACATTCCAA 180
CTCCAGAAATG ATCCCCAATC ACCCTAATCT CAGAATGCTG GAATGATGTC TGTGGCAAA 240
CCCAGGACTC CACACTCGAG 260

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

GAAGCGACCA TTCGTCCAAC AGGTATGGCT GGTTTTGTG CAATGAGAGA ATGTCCACTC 60
GCAATGATGA GCCTGAGAAG GCAAGTCGTC CGTTTGATGT GGATCGCGAT GGTTTTGTTA 120
TGGTGAAAGG TGCCGGGATT CTTATTCTGG AATCACTCGA ACATGCTGAG AAACGTGGAG 180

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

GAATTCGGCC AAAGAGGACT ACACAGAGCC CCTGTTTGGG AATTTGAGAT TCTGTGTCAT 60
GCTGGTTTTT CTTTCAGAAT TGCTTGAAAT CGAGTTCTCT TAGCCACTGG ACACCTAGTT 120
TTCAGGAGAA TGTCCCAAGA TTGTTTATAT ATACAAAATG GCAAAAGTAC TGTTTTTCGA 180
ATTGATAATT CAAGCAAAGG CTTCTCTTTA CTGTCACTGA TTTTITTTTG TTTTATTTT 240
GTTTCCTTGT TTCTATTTCC TTGAAGCTTT GAAGGGAGGA GAAGCAGAAA ATTTTGTTTA 300
TGTTTGTTAA AAATCAGAAC TACTTAATGC TTTTGGCCAC AGCATATTTT CTGTCCTGTT 360
GGAGCCGTTA GGAAGATTAC CTATGTCCTA ATCTTCAACC TGAGAAGATT TTTGACTCTT 420
GTGTCCTACTG TTGATGTGTT GCTTGAGTTC TCAAAGACCT GTGCCAGGT ATTTTAAAAA 480
GTCGTCTATT TCTCGAG 497

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GAATTCGGCC	AAAGAGGCCT	AGCAAAATCA	AATTCAACCC	ATGAGTCACA	GTGCTTTCTT	60
CAACAAGAAA	ACATTGAACA	CAGAAAGCAA	TTGTGAATAT	AAGGACCCCTG	GGAAAATGAT	120
TCGCACGAGG	CCCCACCTTG	CTTCTTCACA	GAAACAACCT	CAGAAATGTT	GCTTATTTAC	180
AGAAAGTTTG	AAGCTGAACC	TAGAAGTGAA	CGGTCAGAAT	GAAAGCAATG	ACACAGAACA	240
GCTTGATGAC	GTGTGTTGGT	CTGGTCAGCT	ATTCAGCCAT	AGCTCTTCTG	ATGCCTGCAG	300
CAAGAATATT	CATACAGGAG	AG				322

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GGCCCACCTG	TGTCCTGGTT	GAGGGTCTCC	AGGGTTCTTT	GGGGCCCGAG	GCCAATGGTG	60
GCAGAGTCTA	CATAGAACTA	TGCTTCGTGG	TGTTCTGGGG	AAAACCTTTC	GACTTGTTGG	120
CTATACTATT	CAATATGGCT	GTATAGCTCA	TTGTGCTTTT	GAATACGTTG	GTGGTGTTGT	180
CATGTGTTCT	GGACCATCAA	TGGAGCCTAC	AATTCAAAAT	TCAGATATTG	TCCTTGCCAGA	240
AAATCTTAGT	CGACATTTT	ATGGTATCCA	AAGAGGTGAC	ATTGTGATTG	CAAAAAGCCC	300
AAGTGATCCA	AAATCAAATA	TTGTAAAAG	AGTAATTGGT	TTGGAAGGAG	ACAAAATCCT	360
CACCACTAGT	CCATCAGATT	TCTTTAAAAG	CCATAGTTAT	GTGCCAATGG	GTCAATGTTG	420
GTTAGAAGGT	GACAATCTAC	AGAATTCTAC	AGATTCCAGG	TGCTAGGCCT	CTTTGGCCGA	480
A						481

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GAATTCGGCC	AAAGAGGCCT	AGGGAAGAGT	GGAACAAAAG	TCAGTCGTAC	ATTCAGCTAC	60
ATCAAGAATA	AAATGTCTAG	CAGCAAGAAG	AGCAAAGAAA	AGGAAAAAGA	AAAAGATAAG	120
ATTAAGGAGA	AGGAGAAAGA	TTCTAAAGAC	AAGGAGAAAG	ATAAGAAGAC	TGTCAACGGG	180
CACACTTTCA	GTTCCATTCC	TGTTGTGGGT	CCCATCAGCT	GTAGCCAGTG	TATGAAGCCC	240
TTCACCAACA	AAGATGCCTA	TACTTGTGCA	AATTGCAGTG	CTTTTGTCCA	CAAAGGCTGC	300
CGAGAAAGTC	TAGCCTCCTG	TGCAAAGGTC	AAAATGAAGC	AGCCCAAAGG	GAGCCTTCAG	360

GCACATGACA CATCATCACT GCCCACC

387

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

GAATTCGGCC	AAAGAGGCCT	AACGCAGCCA	TGGCTCGTGG	TCCCAAGAAG	CATCTGAAGC	60
GGGTGGCAGC	TCCAAAGCAT	TGGATGCTGG	ATAAATTGAC	CGGTGTGTTT	GCTCCTCGTC	120
CATCCACCGG	TCCCCACAAG	TTGAGAGAGT	GTCTCCCCCT	CATCATTTTC	CTGAGGAACA	180
GACTTAAGTA	TGCCCCGACA	GGAGATGAAG	TAAAGAAGAT	TTGCATGCAG	CGGTTTATTA	240
AAATCGATGG	CAAGGTCCGA	ACTGATATAA	CCTACCCTGC	TGGATTCATG	GATGTCATCA	300
GCATTGACAA	GACGGGAGAG	AATTTCCGTC	TGATCTATGA	CACCAAGGGT	CGCTTTGCTG	360
TACATCGTAT	TACACCTGAG	GCGGGCATAA	CACAGCAAGA	CGAGAAGACC	CTATGGAGCT	420
TTAATTTATT	AATGCAACA	GTA				443

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

GAATTCGGCC	AAAGAGGCCT	AAACATCATT	TGTA CTCTAA	TCCAATCAAA	GAAGAAATGA	60
CTGAGTCTAA	GTTCTCTAAG	TACTCTGAAA	TGAGTGAGGA	AAAACGAGCC	AACTTCGTG	120
AAATTGAGCT	CAAAGTTATG	AAGTTTCAGG	ATGAATTGGA	ATCTGGGAAA	AGACCTAAAA	180
AACCAGGCCA	GAGTTTTCAG	GAGCAAGTAG	AACACTACAG	AGATAAACTT	CTTCAACGAG	240
AGAAAAGAGAA	AGAGTTAGAA	AGAGAACGAG	AAAGAGACAA	GAAAGATAAA	GAAAAATTGG	300
AATCTCGCTC	CAAAGACAAG	AAGGAAAAAG	ATGAGTGTA	TCCGACAAGG	AAG	353

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

GAATTCGGCC	AAAGAGGCCT	ACAATTTTTT	GCCTTTTAC	CCTTCTGTCC	TTTAATGCCA	60
TCTCTTTCTC	AATTATTTTC	TCTCATTTTT	TTTCTGAGCA	GACTTATACA	AAAAGGAACA	120
TAAATTAAAT	TTGCCAAATA	TCAAAGAGA	GGAACTTTTT	ATTTTTTATT	TTTTTGGAAC	180
GGAGTCTCAA	TCTGTCTCCC	AGGCTGGAGT	GCAGTGACGC	AATCTCAGCT	CACTGCAACC	240
TCCGCCTCCC	AGTTCAAGAG	ATTCTCTGCC	TCAGCCTCCC	GAGTAGCTGG	GATTACAGGT	300

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ACCCTCTACC ATACTCAGCT AATTTTGTGTA TTTTGTAGTAG AGACTGGTTC ACCATGTGGG      360
CCAGGCTGGT CTCGAACTCC TGACTTCAGG TGTCTGCCT GCTTTGGCCT TCCAAAGTGC      420
TGGGATTATA GGCCTGAGCC ACCACTCTCC ACTGAACCTT TTAATCTTAG AGCAG          475

```

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```

GAATTCGGCC AAAGAGGCCT AGGGGTGTTA ATTAGCTCAG CTGTAGCAAT CATTTTCATAA      60
TGTATATCAA AACATCCAC TGTATACTTT ATACTTTTTT ATAAAAATAA ATATTCTTAC      120
AAAAGGACAG GCGCTGTGTC TGTCTGGCTC ACCATTGTAC CCAATACCCA ACAGGGTGCC      180
AAGTACCCAA TACCCAACAG GGTGCCAAGG AACACAAAAG GCACTCAAAA TATGTTTGTT      240
GATTGGAGTT TACAAGGAAG AAAGGTATTT TCTTATCCCT CTCTTCCCTT CCCACCCAAA      300
CATAGCTTCT TCTAAGAAAA GAAACTGAGG CTGGGCAAGG TTAAGAGCTA GCTCCTGGTA      360
CTTTTGATC CACACTCAGT TTACCTGTGC CTTAAACCAG ACTTCATCAA ACTTCAGTCT      420
TCACAAGTCA CTTCAACATT TTTGCTCTAC CTACTTACTG CCTGTGTAGG CCTCTTTGGC      480
CGAG                                484

```

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

```

GAATTCGGCC AAAGAGGCCT AGTGGGACAT AAGGCTGGAA GGTAGCACAC ACAGCACCAT      60
ATTCTTTTTT ACTTGATGCG GAGTTACTTT GAGTGCTTTT CTCTTACCA AATATATGAG      120
TTCTATTACT ACATTCTTT TCTTTGTTT TTTTAGTGAG ACAGGGTCTC GTTCTGCCTC      180
CCAG                                184

```

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

```

GAATTCGCCC AAAGAGGCCT AGTTTGCGAC TTACTTTTAA TTTCAAATCA GCTGCAGATG      60
TTTGGGAGCC TTCTCGAG                                78

```

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GAATTCGGCC	AAAGAGGCCT	AATGGAAGAT	ATGCTGAAAG	ACTTTCTCCT	TGGAGAACAC	60
TTATTATTGG	TTGGCAACCA	GGGTGTAGGA	AAAAACAAGA	TTGTTGACAC	ATTCCTTCAC	120
CTGCTCAACA	GACCCCGAGA	ATATATTTCAG	CTACACAGGG	ATACCACAGT	ACAAACTCTT	180
ACGCTTCAGC	CTTCGGTTAA	AGACGGACTT	ATTGTATATG	AAGACTCACC	TTTGGTTAAA	240
GCAGTAAAGT	TGGGTCATAT	TCTGGTAGTA	GATGAGGCTG	ACAAAGCTCC	AACAAATGTC	300
ACGTGTATTT	TAAAACTCT	AGTAGAAAT	GGAGAAATGA	TTCTAGCAGA	TGGAAGACGC	360
ATTGTTGCAA	ATTCTGCTAA	TGTGAATGGA	AGAGAAATG	TTGTAGTGAT	TCATCCTGAT	420
TTTAGGATGA	TTGTTCTGGC	AAATAGACCT	GGATTTTCCTT	TCCTAGGCAA	TGATTTCCTC	480
GGTACCTTAG	GTGATATTTT	TAGCTGCCAT	GCAGTTGATA	ACCCCAAACC	CCACTCGGAG	540
CTCGAG						546

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GAATTCGGCC	AAAGGGCCTA	GAGATTTTCAT	GTATTTCTCT	TCACTTCCAA	GAGAGTGGAT	60
AGAATGGAGA	AATCTAGATT	GATCTTTACA	GCTCCAGATA	AAGGGACTAA	AAATATTTGGT	120
TTAAAAATATT	AAAGGTTAAA	GAAAGAGACT	GTTGGTTTCT	TTCAAAGTGA	TTTAAATTTA	180
AACTAGGTTT	TTATTACTAA	GTTTGGGAAA	TGGGGTAACC	ATTTTTTTCT	CATATCAAGG	240
ATATGTACAT	ATTTCCCAT	TCCCATAAT	TAAAAACAAA	CAACTCCCAT	CCACTTCTTA	300
TAAATAGTTC	TTAACTTGGG	CTTAGTAACA	ATGTATATTG	TGCCAGTAAT	ACAGAAAAGG	360
TGGGAGTATA	AAGACCATCC	TGTCCTGTTA	GAATCCTATA	GAACCAAGGT	GCTGGATTAT	420
GGTGGTT						427

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAATTCGGCC	AAAGAGGCCT	AATTTTATTG	AAACTGCTTA	TGTATGTCAA	AGGAGCCAC	60
AACTTCAGCT	ACACAACCTT	TTGTATTGAA	AGAACTCATA	CTTTTGTAG	CTTTTATTC	120
ACATTTAATT	TAAAGTGA	TTAGCACTA	AAATGCCTAG	AAGATTTTAC	TCCAGACCTA	180
TAAGGAAATG	TTTAGTTTTT	ATGAAAAATG	ACAAGTCGAT	GGTTAAACTT	CTCATGTCTT	240
TGGTGCTTTG	GCCCTAATAG	CACTGGACAA	CACCACGACC	ACATGGAAAC	ATATTTTGG	300

AAGCAAACT TTAATTTTAT ATAACGTATG CTATGGAGAA CTCGAG

346

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GAATTCGGCC AAAGAGGCCT AGTGGAGAGT GAAGCTTAAG ACTGCAATTG CAGAAAAAGT 60
CCATGAGGAG AGAAGAAGGA GAAAGGGGG AAGAG 95

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

TTTTTTTTT TTTTITTTAA ATACTTCGCA TACTCTCCAA TGCCCAAAAA TAGCAAGGTG 60
GTAAAAAGAG AATTAGATGA TGATGTTACT GAGTCTGTCA AAGACCTTCT TTCCCAATGA 120
AGACGCAGCT GATGATGCTT TTAAGACAAG TGAACATAAT GTTGATGGCC AGGAAGAGAA 180
AGATACAGAT GTTGAAGAAG GATCTGAAGT CGAAGATGAA AGACCAGCTT GGAACAGTAA 240
ACTACAATAC ATCCTGGCCC AAGTTGGATT TTCTGTAGGT TTAGGAAATG TGTGGCGATT 300
TCCATACCTA TGTCAGAAGA ATGGGGGCGG TGCATATCTT TTACCATATT TAATACTACT 360
TATGGTAATA GGTATTCGCC TTTTITTTCTT GGAACCTCTCT GTGGGTCAA GAACCACTCT 420
CGAG 424

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GCCAAAATCA AGCAAAGTAT GAAGAAAGAT AAAGAAGGGG AAGAAAAAGG GAAGCGAAGA 60
GGATTCCCA GCATCCTGGG ACCCCACGG AGACCAAGCC GTCATGACAA CAGTGCAATT 120
GGCAGAGCCA TGGAATACA GAAGGCGCGC CACCCTAAGC ACTTATCCAC ACCCTCATCT 180
GTGAGTCTTG AACCTCAGGA CTCTGCCAAG TTGCCCCAGA GTGGGTTAGC AAATGAAGGA 240
ACAGACGCTG GATACCTGCC TGCCAATTCC ATGTCTTCTG TAGCTTCAGG GGCCTCTTTT 300
TCCCAGGAAG GAGGGAAAGA GAATGATACA GGATCAAAGC AAGTTGGAGA AACATCAGCA 360
CCTGGAGACA CCTTAGATGT CACCCTCGAG 390

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

```

GAATTCGGCC TTCATGGCCT AGTAGCTGGT ATTTATTCCC CAAAGTAATA ATGTTGAAGT      60
ATGGGTCTCA TCATTCCCAT ACACAGAAAC ACAAACACT TTGATCATAA ACTTTTTTCT      120
TCAGAAAGCCA AACTAACTTG CAGAATAATA GAGCCACTGG TTTAATGTTT CCTCAAGATA      180
GGTTTTAGTG TAAGCTAGTA TTCTGTGTGT TCGTAGAAAT GATTCAATAC CTGCAGCTGG      240
TGAATTAGGA ATTGTATTTG TTGCCTTTTT TATATTAGAT GAGGTGCAAA AATTTTAAATG      300
CTAGTCAGTA TGCACCACCA CAGGAAAGTT AGATCCCATT AGCACTTGAA ACTACAGCTT      360
TGGAAACTTA GGCTAAGTTA ATTTGGATTT GTTACTTGAT TCACCTACTG ACCTTTTCTT      420
TTGTTTGAAG TGCTTATCAG CATAATGAGC TAAGTGTCAT GCATATTTGT GAAGAAACAC      480
CCTTTTGGT CCCTTTGGG ACAGAGAGGT ACTCCTTGAT CTTTATGAAT GACAGGTAC      540
TGTTTTGCCT TATTGCTTAA CTTAATGTAG TGAAATAAAG CAGACGAGGC TCGAG      595

```

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

```

GGCTGATCCG CGTGAACATG GAGGACTTGC GAGAGCAGAC TCACACCCGC CACTATGAAT      60
TGTACCGACG CTGTAAGCTT GAAGAGATGG GGTTCAGGA CACTGACCCT GACAGCAAAC      120
CCTTCAGTCT TCAGGAGACA TATGAAGCAA AAAGGAATGA ATTCCTGGGA GAAGTCAGA      180
AGAAAGAAGA AGAAATGAGA CAAATGTTG TTATGAGAGT GAAGGAGAAA GAAGCTGAAC      240
TTAAGGAGGC AGAGAAAGAG CTTACGAGA AGTTTGACCT TCTAAAGCGG ACACACCAAG      300
AAGAAAAGAA GAAAGTGAA GACAAGGAGA AGGAGCTCGA G      341

```

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

```

GAATTCGGCC TTCATGGCCT ATGCCTTAAT TTGCTGTTT GCCCTCGGAT CTCTGGGTTT      60
GATTTTTGCG TTGACTTTAA ACAGACATAA GTATCCCCTT AACCTGTACC TACTTTTTGG      120
ATTTACGCTG TTGGAAGCTC TGACTGTGGC AGTTGTTGTT ACTTTCTATG ATGTATATAT      180
TATCTGCAA GCTTTCATAC TGACTIONTAC AGTATTTTTT GGTTTGACTG TGTATACTCT      240
ACAATCTAAG AAGGATTTCA GCAAATTTGG AGCAGGGCTG TTTGCTCTTT TGTGGATATT      300
GTGCTGTCA GGATTCCTGA AGTTTTTTTT TTATAGTGAG ATAATGGAGT TGGTCTTAGC      360
CGCTGCAGGA GCGCCACTCG AG      382

```

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

```

GAATTCGGCC TTCATGGCCT ACGAGCCTCA CATCACTTGT ACAAGCCACC TGGGAGAAGT      60
GGCCCTCAGG AAGATCCTAA AACCAATACA CAAATACAAC TTTTTCATTT CATTAAATACA      120
TCAAGTTCAT ATAAGAGTCA AACAGGTAAA AGCAGCATCC CAAACTGTTT TCTCCTCGTA      180
CATGTCAGTT CCACGATCCT CAGTCTCATA AAGTCAGGGA CTAGAGACCA ATGTAATTAT      240
CAATACGTAC CTGCCTTTGA GTGAACCTTC AATGCCAACT AGGAAGGGCG CTTCACAAAC      300
GACGTTATTT GTAATCCTA GGAAGACAAA CACGGGTCAG AACCCATACT CTGCGGGCCT      360
TGAAATGGAA AATCTCTCCT CTAGACAGAC TCATCCTGGC CGTAAATATC AGGAGACTCG      420
AG

```

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

```

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      60
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      120
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      180
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      240
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      300
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      360
NNNNNNNNNN NNCNTTGCAN GNTTTGGTTC CNTTTNTTCC TTGTTTNTTT TTTTGCACAA      420
TATTTCAAGN TTTACNAGGC ATACATCAAT CCAAGTTCGG AATTTTAATT AAGAATTCGG      480
CGTTCATGGC NTAAAAGAAN TTGATGCTAC CCCCAGGAAAT GCCAGAAGAG GANATACATT      540
GAAATAGACN GTGATGAAGA GCCCAGGGGT GAATTACTTT TTNTTCGGGA CANTGAACGC      600
NTTCATAAAA AGCCAAAGTC TGACAAAGAG ACAAGAGTNG CAANTNCAAT GGNTGGANAG      660
ACAGACCGAA AAGAATTTNT GAGGAAGAAA ACCAAAACAA ATCCATNNTC CAGNTCGACA      720
AATNAAGAGA AGNAAANACA GAAGAACTTT ATGATGATGC GGTATAGCCA GAATGTCCGG      780
TCAAAAAATA AGCATTCTCT CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTCGGCC TTCATGGCCT AGGAGGGCCT GTTTCAGAAT TGCTTTAATA GTTCCCTTCC	50
AGTTGAATTT ACCTTTTGCA GGAGCCTCAT CGTCTTCTGG TTCTCCGCCC TCAGGATGCT	120
CTGGGAGCTT CATCTTTTTC TTCTTAGAAT CTGTTTCAAC TTCCGAGTGC CTCCGCTTCC	130
TCTTCCCTGC CCCACGCGTG CCTCTTCCTC ACTGGCGCTG TCCTTGCGCT GCTTCTTCTT	240
CTTGCTCCTC TTCCCTGCAG AGCCATTGGC CTCAGGGACT TCCTCCCCAC CAGCCTCAAG	300
GTCAGCCTCC TGCCTCGAG	319

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GAATTCGGCC TTCATGGCCT AAGAAAAGAC AAGGTCCCCA TAAGAGTGGC GAGAGGAACA	60
GAGCCAGGAC ATCGGAAAGC AAGCCCTGT GTTCCCAAAC CGCAGAAGAG GGAGCTCTGA	120
TGTTAGACAA GCCACCCTCC TACAAGCGAA GGGAAAGTAA CTTTGAGCAA AAATGAGCAA	180
CAGAAAATGA GATCAAGGTC AGATCTCATA CAAAGTTGCA AGATGAAAGA ATGAGCAGCA	240
GAATAACCTC CCTGTGATGT GGAAAGTGTG CCAGGAAAAC AGACCCAAAC GCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GAATTCGGCC TTCATGGCCT AGGGGTTCTT TCTCCTGCAC GATGCCAGGT GGTACTGGAA	60
TCTGCTGAGT GGGATTCCGT GGTGAGGATC ATAAGGGCAA ATTTCAAAGG CTTCTGGCTC	120
CATGAGAAAT TCTTGAAGCA GGGTATCTCA CTGCTAGAGT CTAACGGAAA TGCTTCTTGT	180
GGAGAAGCCC TTTTGTAAGA AGGATGGAGT TGTCTCTGTC CCAGTTTGG CCCTGGGAT	240
TCTGTAGGTG ACGGTCTTAA CTGTGTTCT GTTCTTAGG ACTGTGAGTG GTGGATTAGA	300
AGAGAGATGA GGAGCTGCCA AAAGCAGCTA CACAGAGAAC AGAGTTAGCA AATGGCACCC	360
GAGACAGAAC TATAGCAGAT GCAAGAGCCA AAAACCCACA GCCGCATTGA ATTCTAGACC	420
TGCCTCGAG	429

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GAATTCGGCC TTCATGCCTT GTAACCATCA GGTAGATACA GCACCAACGG TAGTGGCTCT	60
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```

TTATGACTAC ACAGCGAATC GATCAGATGA ACTAACCATC CATCGCGGAG ACATTATCCG      126
AGTGTTTTTC AAAGATAATG AAGACTGGTG GTATGGCAGC ATAGGAAAGG GACAGGAAGG      180
TTATTTTCCA GCTAATCATG TGGCTAGTGA AACACTGTAT CAAGAAGTGC CTCCTGAGAT      240
AAAGGAGCGA TCCCCTCCTT TAAGCCCTGA GGAAAAAACT AAAATAGAAA AATCTCCAGT      306
CCTCGAG                                           307

```

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

```

GAATTCGGCC TTCATGGCCT AGGACCTCGT AGGTCCCTAC AGCACCACAG TGCTCTTCAT      60
CTCTCAGAGG ACTGAACCAC CAGCCAGCAC CAACAGAGAC ACTGTGGAAA GCACAAGGAC      120
CCGACGGGCA CTGAGTGACG AGCAGTGTGC TGCCGTCATC CTTGTGCTGT TTGCTTTCTT      180
TTCCATTTTG ATTGCCTTTA TCATTCAGTA CTTTGTAAAT AAGTGAAAAT ATAACCTTTAT      240
TTTTTAATC TATTACATTT TATTTGTCA TGTACTAAAA TTATTCTGT ATTGCTTTNA      300
TAAAAAACAG TGGCACCTCG AG                                           322

```

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

```

GAATTCGGCC TTCATGGCCT AAAAAACAC ATAATTGAA TCAACACAAC CACCCACAGC      60
CTAATTATTA GCATCATCCC TCTACTATTT TTAAACCAA TCAACAACAA CCTATTTAGC      120
TGTTCCCCAA CCTTTTCCTC CGACCCCTTA ACAACCCCC TCCTAATACT AACTACCTGA      180
CTCCTACCCC TCACAATCAT GGCAAGCCAA CGCCACTTAT CCAGTGAAAC ACTATCACGA      240
AAAAAACTCT ACCTCTCTAT ACTAATCTCC CTACAAATCT CCTTAATTAT AACATTACAA      300
GCCACAGAAC AACTCGAG                                           318

```

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

```

GAATTCGGCC TTCATGGCCT ACAGGAAACA TACAAAGCTG CTCATAGTGG GAGTCTTTTT      60
GCTCATGTTT GTGTGCGGCC TCTTCTTCAC TCGACCTTCA GGCAGCTACT TCATCAGACT      120
GCTGAGTGAC TACTGGATAG TCTTCCCAT CATCGTCGTT GTCGTATTTG AAACCATGGC      180

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TGTATCCTGG	GCCTATGGGG	CCAGGAGGTT	CCTTGCAGAC	CTGACGATCC	TGTTGGGGCCA	240
CCCCATCTCT	CCCATCTTTG	GTGGCTGTG	GCCCCATCTG	TGTCCAGTTG	TGCTGCTAAT	300
CATCTTTGTG	ACCATGATGG	TTCATCTTTG	TATGAAGCCG	ATCACCTACA	TGTCCTGGGA	360
CTCAAGCACC	TCAAAAGAGG	TGCTTCGACC	ATACCCACCG	TGGGCACTGC	TCTTGATGAT	420
CACCCTTTT	GCCATTGTCA	TCCTCCCAT	CCCTGCATAC	TTGTATACT	GCCGCATACA	480
TAGGATTCCC	TTCAGGCCCA	AGAGCGGAGA	CGGGCCTATG	ACAGCCTCCA	CATCCCTACC	540
CCTAAGTCTC	GAG					553

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GAATTCGGCG	TTCATGGCCT	AGTAGAGAAG	ANNNTATTGC	NGTGACAATG	AGGTTTCTAC	60
GTTCAGTGGC	AAGAGTTTTT	GTTATTCTGA	GTGTGGAAAT	GGCTTCATCC	AAAAAGAAAA	120
ACAACCTTAT	TCCACAGCCA	ATTGGAAT	GCAAGCGTGT	ATTCCAAGCA	TTGCTACCTT	180
ACGCTGTGGA	AGAATTGTGC	AACGTAGCAG	AGTCACTGAT	TGTTCTGTG	AGAATGGGGA	240
TTGCTCGTCC	AACTGCACCA	TTTACCCTGG	CTAGTACTAG	CATAGATGCC	ATGCAGGGCA	300
GTGAAGAATT	ATTTTCAGTG	GAACCACTAC	CACCACGACC	ATCATCTGAT	CAGTCTAGCA	360
GCTCCAGTCA	GTCTCAGTCA	TCCTACATCA	TCAGGAATCC	ACAGCAGAGG	CGCATCAGCC	420
AGTCACAGCC	CGTTCGGGGC	AGAGATGAAG	AACAGGATGA	TATTGTTTCA	GCAGATGTGG	480
AAGAGGTTGA	GGTGGTGGAG	GGTGTGGCTG	GAGAAGAGGA	TCATCATGAT	GAACAGGAAG	540
AACACAGGAA	GCTCGAG					557

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTCGGCC	TTCATGGCCT	AAAAAAGTCA	GCCAGGTGTG	GTGATGTGCG	CCTGTGGTCC	60
CAGGTATTCA	CGAGCTGAGG	TGGGAGGATC	ACCTCAGCCC	GGGAGGTGGA	GGTTGCAGTG	120
AGCCCATATC	CCGCCACTGC	ACTCCAACCT	GGGAGACAGA	GCGAGACCCT	GTCTCCAAAA	180
AAAAAAAAAA	AAATCCGGG	ATCTATTTAT	GTAACCTACTA	GAATCTTAAG	TTCAGAATTT	240
ACTCCATAAG	AGTATATAAA	AACTTACTG	TGATTTTATC	CATGTTTTTC	CTAATATATA	300
ATAGGTCTAA	GTCTTGTA	TTTCTGTCCT	GTCCACAGAG	CCTTGAAAT	AATTTAGAGC	360
TCAGTCATT	AGTTTGGATT	TATGTATAAA	TTGAAATATA	TTAATTACTT	ATTATAGT	420
CAGCTCGAG						429

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear